

PS Disclosure; Page 2; 26pp; English.

XX

CC The present invention describes nucleic acids and proteins designated
CC wingless 1 (wt-1), which are involved in the development of Alzheimer's
disease. The nucleic acids have a variety of uses for preventing,
diagnosing and treating Alzheimer's disease. For example, nucleic acids
(or vectors) encoding wt-1 may be administered to treat Alzheimer's
disease by rectifying mutations or deletions in a patient's genome that
affect the activity of wt-1 by expressing inactive proteins or to
supplement the patients own production of wt-1 polypeptides. Conversely,
anticancer nucleic acid molecules may be administered to down regulate
wt-1 expression by binding with the cells own wt-1 genes and preventing
their expression. The nucleic acid probes in diagnostic assays (e.g. polymerase
chain reactions (PCR)) to detect and quantitate the presence of similar
nucleic acid sequences in samples, and hence which patients may be in
need of restorative therapy. They may also be used to study the
expression and function of wt-1 polypeptides and their role in the
pathology of Alzheimer's and in normal metabolism. Anti-wt-1 antibodies
and antagonists may also be used to down regulate wt-1 expression
and activity, and increase rates of apoptosis. The present sequence
represents the human int-1 (mammalian ortholog) protein encoded by the
GENBANK accession # XJ3672 given in 2356; from the present invention.
The present sequence is not given in the specification but is derived
from the GENBANK number given.

CC Sequence 370 AA:

Query Match Best Local Similarity Score 2036: DB 20; Length 370;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGCLWALLPGVNSATLLAALPAALAAANSSGKAWVNVASSTNLITSKSLQVLEPS 60
DB 1 MGCLWALLPGVNSATLLAALPAALAAANSSGKAWVNVASSTNLITSKSLQVLEPS 60

QY 2 Y 61 LQLLSKQRLLRNPGLHSVGGLQSRVKEKLFENKWNPTAPGPHFLFGKIVNRS 120
DB 61 LQLLSKQRLLRNPGLHSVGGLQSRVKEKLFENKWNPTAPGPHFLFGKIVNRS 120

QY 121 CTCCTATTAATSAVTHVASSCISCTTTC 370; Length 370;
DB 121 CTCCTATTAATSAVTHVASSCISCTTTC 370

QY 181 GREEFVSGESEKRDPEFLNLNEARTVFSMPLKIRKHS 345
DB 181 GREEFVSGESEKRDPEFLNLNEARTVFSMPLKIRKHS 345

QY 241 AWYVULRFDGASVYEGNGNSNARFLLERPAKSHSPHNSFEKSENCF 350
DB 241 AWYVULRFDGASVYEGNGNSNARFLLERPAKSHSPHNSFEKSENCF 350

QY 301 YSGRLGAGAAGRNNSSPALGEGELONGRHRHFKIQTETCNCFTHWCHSCRN 360
DB 301 YSGRLGAGAAGRNNSSPALGEGELONGRHRHFKIQTETCNCFTHWCHSCRN 360

QY 361 THIRVHECL 370
DB 361 THIRVHECL 370

RESULT 2
AYY70733
ID AYY70733 standard; Protein; 370 AA.
XX
AC AYY70733;
XX DT 24-JUL-2000 (first entry)
XX DE Human Wnt-1 protein.
XX KW Human Wnt-1; Wnt antagonist; contraceptive; contraceptive vaccine;

KW monoclonal antibody; Wnt signalling.

XX Home sapiens.

XX WO2002155-A1.

PN PD 26-APR-2000.

PR 15-MT-1998; 96US-014355.

XX PA (HAKU) HARVARD COLLEGE.

XX McMahon AP, Parr BA, Vainio S;

DR WPI: 2002-3-2445/27.

FT Contractive composition for inhibiting oocyte development in a female primate comprising a Wnt polypeptide antagonist.

XX Example 3; Page 23; 57pp; English.

CC The patient discloses a method of female primate oocyte development comprising administering an antagonist of a Wnt polypeptide inhibiting oocyte development. Wnt polypeptides are useful for promoting maturation of an immature oocyte. Wnt polypeptides are also useful for increasing the number of mature oocytes and to enhance oocyte viability. The present sequence is the human Wnt-1 protein. Soluble fragments of Wnt polypeptides have the ability to inhibit Wnt signalling, e.g., by blocking binding of a naturally-occurring Wnt protein to its receptor. They may be used to generate monoclonal antibodies which can inhibit oocyte development.

XX Sequence 370 AA:

Query Match Best Local Similarity Score 2036: DB 21; Length 370;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGCLWALLPGVNSATLLAALPAALAAANSSGKAWVNVASSTNLITSKSLQVLEPS 60
DB 1 MGCLWALLPGVNSATLLAALPAALAAANSSGKAWVNVASSTNLITSKSLQVLEPS 60

QY 181 GREEFVSGESEKRDPEFLNLNEARTVFSMPLKIRKHS 345
DB 181 GREEFVSGESEKRDPEFLNLNEARTVFSMPLKIRKHS 345

QY 241 AWYVULRFDGASVYEGNGNSNARFLLERPAKSHSPHNSFEKSENCF 350
DB 241 AWYVULRFDGASVYEGNGNSNARFLLERPAKSHSPHNSFEKSENCF 350

QY 301 YSGRLGAGAAGRNNSSPALGEGELONGRHRHFKIQTETCNCFTHWCHSCRN 360
DB 301 YSGRLGAGAAGRNNSSPALGEGELONGRHRHFKIQTETCNCFTHWCHSCRN 360

QY 361 THIRVHECL 370
DB 361 THIRVHECL 370

RESULT 3
AYY70733
ID AYY70733 standard; Protein; 370 AA.
XX
AC AYY70733;
XX DT 24-JUL-2000 (first entry)
XX DE Human Wnt-1 protein.
XX KW Human Wnt-1; Wnt antagonist; contraceptive; contraceptive vaccine;

RESULT 3
AYY70733
ID AYY70733 standard; Protein; 370 AA.
XX
AC AYY70733;
XX DT 24-JUL-2000 (first entry)
XX DE Human Wnt-1 protein.

XX AAY57594;
 AC XX
 XX DT 02-MAR-2000 (first entry)
 DE XX Human Wnt-1 protein.
 KW XX Wnt-1; neuronal growth; differentiation; regeneration; dorsal neural progenitor cell; neurodegenerative disease; Parkinson's disease; amyotrophic lateral sclerosis; diffuse Lewy body disease; cortical-basal ganglionic degeneration; Hallervorden-Spatz disease; myoclonic epilepsy.
 XX OS Homo sapiens.
 XX PN WO9957248-A1.
 XX PD 11-NOV-1999.
 XX PR 30-APR-1998: 98WO-US08716.
 XX PR 30-APR-1998: 98WO-US08716.
 XX PA (HARD) HARVARD COLLEGE.
 XX PT McMahon AP, Lee SK, Takada S;
 XX DR WPI: 2000-06-21A5/5.
 XX N PCTB: RA247788.
 XX PT Enriched populations of mammalian neural precursor cells for treating Parkinson's disease.
 XX PS Claim 6; Page 4; 57PP; English.
 XX CC The present invention describes an enriched population of mammalian neural precursor cells committed to a cell fate, the cells being characterised in that they exhibit a stem cell phenotype in the presence of Wnt polypeptide but not in the absence of the Wnt polypeptide. The enriched population of dopaminergic neuron precursor cells can be used in a method for treating Parkinson's disease. The enriched population of dorsal neural precursor cells can be used to induce neuronal regeneration in an adult mammal suffering from a neurodegenerative disorder. The disorder that can be treated is Parkinson's disease, Amyotrophic lateral sclerosis, diffuse Lewy body disease, cortical-basal ganglionic degeneration, Hallervorden-Spatz disease or crochetic epilepsy. The present sequence represents the human Wnt-1 protein.
 XX SQ Sequence 370 AA:
 Query Match 100.0%; Score 2036; DB 21; Length 370;
 Best Local Similarity 100.0%; Pred. No. 3.9e-15;
 Matches 370; Conservative 0; Mismatches 0; Index 0; Gaps 0;
 QY 1 MGILWALLPQWVATILLALALPALAANSGRGMWIVNVAASSNLITSKSOLVLEPS 65
 1 MGILWALLPQWVATILLALALPALAANSGRGMWIVNVAASSNLITSKSOLVLEPS 65
 QY 61 LQLLSRKPLRLTRNGTILHSVGLOSSAVRECKWFLRNCRNCPTAGPHLEKINRG 120
 61 LQLLSRKPLRLTRNGTILHSVGLOSSAVRECKWFLRNCRNCPTAGPHLEKINRG 120
 Db 121 CRETAFIAITAGVHVSVARSEGGESTCSDYRRGPGDWIIGGGSNDNIDFGKLP 180
 QY 181 GREFDSEFEGKDLRLTMNHNRAGRITVESEMCEKCHOMSGCTVTCRRLTUP 240
 181 GREFDSEFEGKDLRLTMNHNRAGRITVESEMCEKCHOMSGCTVTCRRLTUP 240
 QY 241 AVGDYLQRDFDASKRYLGGSRARRAELRLEPEPAHPSPSHDLYFEKSPNCT 300
 241 AVGDYLQRDFDASKRYLGGSRARRAELRLEPEPAHPSPSHDLYFEKSPNCT 300
 Db 241 AVGDYLQRDFDASKRYLGGSRARRAELRLEPEPAHPSPSHDLYFEKSPNCT 300
 QY 361 YSGFISTATAGA:SSPAALACELLGCGRGKPTCIVHNRTHWCVHS:RNC 360
 DB 361 YSGFISTATAGA:SSPAALACELLGCGRGKPTCIVHNRTHWCVHS:RNC 360
 QY 361 THRVHEI 370
 DB 361 THRVHEI 370
 PR RESULT 4
 AAB19745 5 standard residues: -73 AA.
 XX PR AAB19785;
 XX DT 19-FEB-2001 (first entry)
 XX DE Human Wnt-1 protein involved in kidney tubulogenesis.
 XX PR 08 APR-1997: 98WO-US0745.
 XX PS Homo sapiens.
 XX PR K200005164-A1.
 XX PA (HARD) HARVARD COLLEGE.
 XX PT McMahon AP, Rister A, Vaithe S;
 XX DR WPI: 2000-07-14A6/6.
 XX N PCTB: RA247784.
 XX PT Inducing kidney tubule formation in a post-natal animal, involves administering a substantially pure Wnt polypeptide or its agonist - claim 18; page 2-9; 57PP; English.
 XX PS The present sequence is that of human Wnt-1, a Wnt-1 that acts as a trigger to start an integrin program in mesenchymal cells which leads to the formation of complex nephron-like structures. Kidney tubule formation in a post-natal animal is stimulated by administering a Wnt polypeptide or a nucleic acid encoding it. The Wnt-1 class polypeptide is selected from Wnt-4 or a Wnt-1 class protein such as Wnt-1, Wnt-2, Wnt-3a, Wnt-7a and Wnt-8 (see ADL78659). A Wnt-1 class polypeptide is a Wnt polypeptide that transmits signals in cells in culture. The method is preventative or therapeutic and is administered to a juvenile or adult mammal (including humans) for the treatment of kidney disorders including chronic renal failure, renal cell carcinoma, polycystic kidney disease, stroke, obstructive uropathy, and virus, especially HIV-1, induced neuropathy (claimed).
 XX SQ Sequence 370 AA:
 Query Match 99.5%; Score 2026; DB 21; Length 470;
 Best Local Similarity 99.7%; Pred. No. 3.9e-191;
 Matches 359; Conservative 0; Mismatches 0; Index 0; Gaps 0;
 QY 1 MGILWALLPQWVATILLALALPALAANSGRGMWIVNVAASSNLITSKSOLVLEPS 65
 1 MGILWALLPQWVATILLALALPALAANSGRGMWIVNVAASSNLITSKSOLVLEPS 65
 Db 61 LQLLSRKPLRLTRNGTILHSVGLOSSAVRECKWFLRNCRNCPTAGPHLEKINRG 120
 QY 1 LQLLSRKPLRLTRNGTILHSVGLOSSAVRECKWFLRNCRNCPTAGPHLEKINRG 120

Sequence		468 AA;
QY	61 HQLRSRKQRLLRQNPSILHSVSGLQSAVRECKWKRERNRWNPTARGPHFLFGKVNR	3 120
Db	121 CRETAFIFAITASAGVTHSVAWSVARCSGSESTCCTDYHRKGPGPWHMGCSUNIDFGLF	180
Db	121 CRETAFIFAITASAGVTHSVAWSVARCSGSESTCCTDYHRKGPGPWHMGCSUNIDFGLF 180	180
QY	181 GREYFDGSGERGRDRFLRMNHLHNNEAGRITVFSERMRECKCHGMGSCVTWCWMRPLTR	240
Db	181 GREYFDGSGERGRDRFLRMNHLHNNEAGRITVFSERMRECKCHGMGSCVTWCWMRPLTR	240
QY	241 AVGDYLDRDGFASRVLYGRRGSNRASRERLEPDPAHKPSPHDLVYFEKSPNFT	300
Db	241 AVGDYLDRDGFASRVLYGRRGSNRASRERLEPDPAHKPSPHDLVYFEKSPNFT	300
QY	301 YSGRIGTACTAATRACNSSSPALDGCCELLCGGHRRTQTYRTERCNCFHWCHSCRNC	360
Db	301 YSGRIGTACTAATRACNSSSPALDGCCELLCGGHRRTQTYRTERCNCFHWCHSCRNC	360
QY	361 THTRLHEL 370	
Db	361 THTRLHEL 370	
RESULT 5		
ABB61007	ID ABB61007 standard; Protein: 468 AA.	
AC	ABB61007;	
XX	DT 26-MAR-2002 (first entry)	
XX	DE Drosophila melanogaster polypeptide SEQ ID NO 9813.	
KW	kw; drosophila; developmental biology; cell signalling; insecticide; pharmaceutical.	
KW	kw; drosophila; melatogaster.	
XX	PS WO200171042-A2.	
XX	PD 27-SEP-2001.	
XX	PF 23-MAR-2001; 2001WO-US09231.	
PR	23-MAR-2000; 2000US-191637P.	
PR	11-JUL-2000; 2000US-0614150.	
PA	(PEKE) PE CORP NY.	
XX	Venter JC, Adams M, Li PW, Myers EW;	
DR	WPI: 2001-656860/75.	
N-PSDB:	ABL05110.	
PA	(PEKE) PE CORP NY.	
XX	New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions.	
PS	Disclosure: SEQ ID NO 9813; 21pp + Sequence listing; English.	
XX	The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL1616-ABL3051), expressed DNA sequences (ABL0140-ABL6175) and the encoded proteins (ABL5737-ABL2072).	
CC	The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.	
XX		
QY	31 SGR---WWGVNVNVAASNLTDSSKSHVLPPL-QLSRKFRKIRKPNGLHVSQG	84
Db	30 SGRRGSMWGWIAKVGEPNNI----TPIMDPDPAHSLRKKRVRTPNGVILAWK	84
QY	85 GLOSSVRECKWKRFRNIRRNWNPTE--ACPQHFGKVNRCORETAFFAITSAGVTHSAR	141
Db	85 GANAIASECOHQRFRNRWNGSTRNFSRNSRQKNLFGKWDGCRETSFYTAISAVHSAR	144
QY	142 SCGSGSIESTDY--RRGP-----GGPDMHWGCSNILEJ3KLEGREFDGSSE	189
Db	145 ACSEGTISCTSDYSHOSRQPAHQNSQAVGSGVWRWEGWQMSNSLGHPSFKEREDVGE	204
QY	190 KGDRLFMLNHNNNEAGRITVFSERMRECKCHGMGSCVTWCMPK-PLTAVGDLVDR	249
Db	205 RGRNLREKMNHNNEAGRHAQVOAMEROCKCHGMGSCVTWCMLRANFRVSDNLKAR	264
QY	250 FDGASRVLGN-----RGSNRASRELL-----	272
Db	265 FDGAIFRQVGTNSLRATNALAPVSPNAASNSVGSNLIPQSGIVYSEEERMLNDHMPD	324
QY	273 -----	
Db	325 ILLENSHEISKHHNPMPNSLPOAGGORGRRRQRGRKHNVPHLNUHNPENPKPGS	384
QY	287 HDLVYFEKSPNFTCTYSGRLTAGTAGRACNSSSPALDGCCELLCGGHRRTQTYRTERCN	346
Db	385 KDLVYLEHSPSPCCKEKLNRQGILGHGRCNETSLGWGQGLMCGRJYHDEUVVWERKA	444
QY	347 CTFHMCVCHVSCRNCNTTRVHEL 370	
Db	445 CTFHMCVCHVSCRNCNTTRVHEL 468	
RESULT 6		
XX	ID AY57596 standard; Protein: 352 AA.	
AC	AY57596;	
XX	DT 02-MAR-2000 (first entry)	
XX	DE Murine Wnt-3a protein.	
PA	XX	
XX	Wnt-1; neuronal growth; differentiation; renebration; dorsal neural progenitor cell; neurodegenerative disease; Parkinson's disease; amyotrophic lateral sclerosis; diffuse Lewy body disease; cortical-basal ganglion degeneration; Hallervorden-Spatz disease; myoclonic epilepsy.	
DS	DS Mus sp.	
XX	W095957248-A1.	
PN		
XX	PD 11-NOV-1999.	
XX	PP 30-APR-1998; 98WO-US08716.	
PR	30-APR-1998; 98WO-US08716.	
XX	PA (HARD) HARVARD COLLEGE.	
XX	PT McMahon AP, Lee SK, Takada S;	
XX	WPI: 2000-062145/05.	
DR	N-PSDB; AAZ47790.	
XX	PT Enriched populations of mammalian neural precursor cells, for treating	

AC AAY41719;
 XX
 DT 07-DEC-1999 (first entry)
 XX
 DE Human PR0864 protein sequence.
 XX
 KW Human; PRO; EST; expressed sequence tag; PCR primer; hybridization;
 KW probe; blood coagulation disorder; cancer; cellular adhesion disorder;
 XX
 OS Homo sapiens.
 XX
 PN WO9946281-A.
 XX
 PD 16-SEP-1999.
 XX
 PF 08-MAR-1999: 99WO-US05028.
 XX
 PR 10-MAR-1998: 98US-0077450.
 PR 11-MAR-1998: 98US-0077632.
 PR 11-MAR-1998: 98US-0077641.
 PR 11-MAR-1998: 98US-0077549.
 PR 12-MAR-1998: 98US-0077791.
 PR 13-MAR-1998: 98US-0078004.
 PR 17-MAR-1998: 98US-0078020.
 PR 20-MAR-1998: 98US-0078886.
 PR 20-MAR-1998: 98US-0078910.
 PR 20-MAR-1998: 98US-0078936.
 PR 20-MAR-1998: 98US-0078939.
 PR 25-MAR-1998: 98US-0079294.
 PR 26-MAR-1998: 98US-0079656.
 PR 27-MAR-1998: 98US-0079663.
 PR 27-MAR-1998: 98US-0079664.
 PR 27-MAR-1998: 98US-0079689.
 PR 27-MAR-1998: 98US-0079726.
 PR 27-MAR-1998: 98US-0079785.
 PR 30-MAR-1998: 98US-0079925.
 PR 30-MAR-1998: 98US-0079923.
 PR 31-MAR-1998: 98US-0000105.
 PR 31-MAR-1998: 98US-0000165.
 PR 31-MAR-1998: 98US-0000194.
 PR 01-APR-1998: 98US-0000327.
 PR 01-APR-1998: 98US-0000328.
 PR 01-APR-1998: 98US-0000333.
 PR 01-APR-1998: 98US-0000334.
 PR 08-APR-1998: 98US-0081049.
 PR 08-APR-1998: 98US-0081070.
 PR 08-APR-1998: 98US-0081195.
 PR 09-APR-1998: 98US-0081293.
 PR 09-APR-1998: 98US-0081299.
 PR 15-APR-1998: 98US-0081817.
 PR 15-APR-1998: 98US-0081838.
 PR 15-APR-1998: 98US-0081952.
 PR 15-APR-1998: 98US-0081955.
 PR 21-APR-1998: 98US-0082568.
 PR 21-APR-1998: 98US-0082569.
 PR 22-APR-1998: 98US-0082700.
 PR 22-APR-1998: 98US-0082704.
 PR 22-APR-1998: 98US-0082708.
 PR 23-APR-1998: 98US-0082736.
 PR 27-APR-1998: 98US-0083322.
 PR 29-APR-1998: 98US-0083392.
 PR 29-APR-1998: 98US-0083495.
 PR 29-APR-1998: 98US-0083496.
 PR 29-APR-1998: 98US-0083499.
 PR 29-APR-1998: 98US-0083500.
 PR 29-APR-1998: 98US-0083545.
 PR 29-APR-1998: 98US-0083554.
 PR 29-APR-1998: 98US-0083558.

PR 29-APR-1998: 98US-0083559.
 PR 30-APR-1998: 98US-0083742.
 PR 05-MAY-1998: 98US-0084366.
 PR 06-MAY-1998: 98US-0084414.
 PR 06-MAY-1998: 98US-0084598.
 PR 07-MAY-1998: 98US-0084598.
 PR 07-MAY-1998: 98US-0084627.
 PR 07-MAY-1998: 98US-0084637.
 PR 07-MAY-1998: 98US-0084639.
 PR 07-MAY-1998: 98US-0084640.
 PR 07-MAY-1998: 98US-0084643.
 PR 13-MAY-1998: 98US-0085323.
 PR 13-MAY-1998: 98US-0085338.
 PR 13-MAY-1998: 98US-0085339.
 PR 15-MAY-1998: 98US-0085573.
 PR 15-MAY-1998: 98US-0085580.
 PR 15-MAY-1998: 98US-0085582.
 PR 15-MAY-1998: 98US-0085589.
 PR 15-MAY-1998: 98US-0085597.
 PR 15-MAY-1998: 98US-0085700.
 PR 15-MAY-1998: 98US-0085704.
 PR 15-MAY-1998: 98US-0085708.
 PR 18-MAY-1998: 98US-0087106.
 PR 22-MAY-1998: 98US-0087392.
 PR 22-MAY-1998: 98US-0684414.
 PR 22-MAY-1998: 98US-0684416.
 PR 22-MAY-1998: 98US-0684466.
 PR 28-MAY-1998: 98US-0087098.
 PR 28-MAY-1998: 98US-0087106.
 PR 28-MAY-1998: 98US-0087208.
 PR 30-JUL-1998: 98US-0084651.
 PR 11-SEP-1998: 98US-0101038.

XX
 PT (PCTH) GENENTECH INC.
 XX
 PT Wood WI, Goddard A, Gurney A, Yuan J, Baker R, Ten J,
 XX
 PR N-1511, RA234081.
 XX
 PT New secreted and transmembrane polypeptides and their poly nucleotides,
 PT useful for treating blood coagulation disorders, cancers and cellular
 PT adhesion disorders.

XX
 PS Claim 12; Fig 63; 530pp; English.

XX
 OC The present invention describes secreted and transmembrane polypeptides
 OC and their poly nucleotides. The nucleotide sequences are useful as
 OC sources or probes. Primers for chromosome mapping and for generation
 OC of antisense sequences. They can also be used to clone the transmembrane
 OC animals. The proteins can be used to treat a variety of diseases and
 OC disorders, depending on their function. Diseases that may be treated
 OC include blood coagulation disorders, cancers and cellular adhesion
 OC disorders. They may also be used to raise antibodies. RA233811 to
 OC AA234338, and AAY41685 to AAY4174 represent polynucleotide and
 OC polypeptide sequence given in the exemplification of the present
 OC invention.

XX
 Sequence 551 AA:

Query Match Score 41/38; Score 84.0; 58 24; Iter: 12; 351:
 Best local similarity 44.8%; Prei. No. 2, 1e-75; Mismatches 123; Pos: 20; 348 4;

Matches 161; Conservative 55; Mismatches 123; Pos: 20; 348

QY 14 MLLALALPAALANNSSRGGVIVWAASNTLDSRSQLVLESLVLSRKQRFLIR 73
 Db 9 SRLMVEAVSAASN---WILYLAKLSSVGSEETCE---KJGKLQROWQCK 58

QY 74 QNGILUSVSGLGSAVECKRKRNRCPAPGPHFEKTKR3FETAFIAITSA 133
 Db 59 RNLNEVMUSVRGAQIAEIQYQFRRNRMCSILDSPVFSQVYQCFEARVVAISSA 118

QY 134 GVTBSVARSCSEGSISETCDYRRGGPGPDWHW3GCSNDPGRFLGREFVDSGEKSR- 192
 ||| :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
 Db 119 GVAFAVTRACSGEELKRCGCDRTVHGYSPQFOWSGCNSIAYGVAFSQFDVRSRGK 178
 QY 193 -DIFLMILHNNEARTRTTFSEROCKHOMSCVTRTWMRLEPT 250
 ||| :|||:|||:|||:|||:|||:|||:|||:
 Db 179 ASSRALMHNNEAERKAATIIRVECKCHGVSGCEVKTCARAVPFVGHALKEF 238
 QY 251 DGASVLYKONRSNRASRAELREPPDAHKPSPHFVWFEDKSNPCTYSGLGIACT 310
 ||| :|||:|||:|||:|||:|||:|||:
 Db 239 DGATEVERRVASSRA-----LVPNAQPKHIDLVYLSPRFQDMMSGVAT 291
 QY 311 AGRAGNSSSPALEGELCGRHRIRQRVIEBNGTHWCHNNSCRNTHTHVHEC 369
 ||| :|||:|||:|||:|||:|||:
 Db 292 RGRTRNKTSAIDGELCCGSRSHFTAOVLAEPISCKHWSFVKRCFVQFLVHLIC 353
 RESULT 9
 AAB44275 ID AAB44275 Standard; Protein: 351 AA.
 XX AC AAB44275;
 XX DT 08 FEB 2001 (first entry)
 XX DE Human PRO664 (UNJ426) protein sequence SEQ ID N:226.
 XX KW Human; secreted protein; transmembrane protein; PRO; EST; cytosolic; expressed sequence tag; detection; cancer.
 XX OS Homo sapiens.
 XX PN WO20053756-A2.
 XX PD 14-SEP-2000.
 XX PF 18-FEB-2000; 200304-0504341.
 XX PR 08-MAR-1999; 9940-0505028.
 PR 12-MAR-1999; 995S-0-23457.
 PR 29-MAR-1999; 9940-012573.
 PR 21-APR-1999; 990S-013032.
 PR 28-APR-1999; 990S-013145.
 PR 14-MAY-1999; 990S-0134287.
 PR 23-JUN-1999; 990S-0141037.
 PR 26-JUL-1999; 990S-0145658.
 PR 29-OCT-1999; 990S-0162506.
 PR 30-NOV-1999; 990S-0528313.
 PR 02-DEC-1999; 9940-0528551.
 PR 07-DEC-1999; 9940-0528555.
 PR 16-DEC-1999; 9940-0530055.
 PR 30-DEC-1999; 9940-0531243.
 PR 05-JAN-2000; 200040-0500219.
 PR 06-JAN-2000; 200040-0500277.
 PR 06-JAN-2000; 200040-0500376.
 XX PA (GETH) GENENTECH INC.
 XX PI Astkenazi AJ, Baker KP, Botstein D, Testyovers L, Eaton DL, Fong S, Gerber H, Gerritsen ME, Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Hillian RJ, Goldard A, Godowski PJ, Grimaldi CJ, Gurley AL, Roy MA, KJ Javin IJ, Kuo SS, Napier MA, Pan J, Poni NF, Roy MA, PI PI Shelton DL, Stewart TA, Tumas D, Williams PM, Wood WI; DR WPI: 2000-611443/58.
 XX DR N-FSDB; AAC78505.
 XX PT Novel PRO polypeptides and polynucleotides used in detection methods, to target bioactive molecules to specific cells, and to modulate cellular activities.
 XX PS Claim 12; Fig 83; 535pp; English.

XX XX ACT78458 to AAC78599 represent poly nucleotide and EST (expressed sequence tag) sequences which encode secreted transmembrane PRO polypeptides. The PRO polynucleotides and polypeptides have cytotoxic activity. The polynucleotides and polypeptides can be used for detecting the presence of PRO polypeptides in samples, for linking bioactive molecules to cells and for modulating biological activities of cells, using the polypeptides for specific targeting. The polypeptide targeting can be used to kill the target cells e.g. for the treatment of cancers. The polypeptide pairs provide specific targeting of bioactive molecules to cells. AAC78600 to AAC78987 represent PCR primers and probes used in the isolation of the PRO polypeptides sequences.

XX SQ Sequence and AA:

query Match length: 41 341 Score: 8430 Up: 21 Down: 3670
 best: local similarity: 44.9%; pred.: No. 210; mismatch: 22%; gaps: 4;
 matches: 161; conservative: 44.9%; mismatches: 22%; gaps: 2%; gaps: 4;

QY 114 TLLAKALPAALAGNSGKGIVNVAASSNLHNSKLAVIENSLISKPLKLR 73
 Db 9 SLRLNAYFVSAASN---WLYLAKLSSWSISREFEE---KIKLILQVQMK 58
 QY 144 GTHSAAVSSESLCTCILKTKPGRPHWMSJESMT3P1KPNHESERK 133
 Db 119 GVAFAVTRACSGEELKRCGCDRTVHGYSPQFOWSGCNSIAYGVAFSQFDVRSRGK 178
 QY 153 -DIFLMILHNNEARTRTTFSEROCKHOMSCVTRTWMRLEPT 250
 Db 179 ASSRALMHNNEAERKAATIIRVECKCHGVSGCEVKTCARAVPFVGHALKEF 238
 QY 251 DGASVLYKONRSNRASRAELREPPDAHKPSPHFVWFEDKSNPCTYSGLGIACT 310
 Db 292 RGRTRNKTSAIDGELCCGSRSHFTAOVLAEPISCKHWSFVKRCFVQFLVHLIC 353
 RESULT 10
 AAY5270 ID AAY5270 Standard; Protein: 351 AA.
 XX AC AAY5270;
 XX DT 05-JUN-2000 (first entry)
 XX DE Wnt-4AF and Wnt-5c homolog polypeptide #1.
 XX KW Wnt; Wnt-4AF; Wnt-5C; frizzled gene; membrane protein; diagnostic; therapeutic; human.
 XX OS Homo sapiens.
 XX PN WO200512117-A1.
 XX PR 03-AUG-1999; 9940-0529045.
 PR 31-AUG-1999; 990S-0-9844.
 PR 31-AUG-1999; 990S-0-98453.
 PR 30-SEP-1999; 990S-0-98452.
 PR 03-DEC-1999; 990S-0-11565.
 PR 03-DEC-1999; 990S-0-11566.
 PR 03-DEC-1999; 990S-0-11567.
 PR 03-DEC-1999; 990S-0-11568.

OS Homo sapiens.
 CC proteins can be used to determine the presence of tumours and also
 CC susceptibility to tumour development, particularly adrenal, lung, colon,
 CC breast, prostate, rectal, cervical, or liver tumours, in mammalian
 CC subjects. The oligonucleotide probes specific to the PRO nucleic acids
 CC can be used for genotypic analysis of individuals with hereditary disorders.
 XX Sequence 451 AA:
 SQ Query Match, Similarity 44.8%; Prcd. No. 2, 1e-57;
 Best Local Similarity 55.5%; MisMatches 121; Idxes 20; Gaps
 Matthes 161; Conservative 55; MisMatches 121; Idxes 20; Gaps
 QY 14 TILKALALPAMIAANSSRPAVIVVASSINNLTDKSLQWIFSTJLRSKURFLR 73
 PR ;
 PR 14 MAR 2000; 2000US-18932P.
 PR ;
 PR 15 MAR 2000; 2000WO-US06884.
 PR ;
 PR 21 MAR 2000; 2000US-19028P.
 PR ;
 PR 21 MAR 2000; 2000US-19107P.
 PR ;
 PR 21 MAR 2000; 2000US-19104P.
 PR ;
 PR 21 MAR 2000; 2000US-19131P.
 PR ;
 PR 29 MAR 2000; 2000US-19303P.
 PR ;
 PR 29 MAR 2000; 2000US-19305P.
 PR ;
 PR 30 MAR 2000; 2000WO-US08439.
 PR ;
 PR 04 APR 2000; 2000US-19444P.
 PR ;
 PR 04 APR 2000; 2000US-19454P.
 PR ;
 PR 11 APR 2000; 2000US-19597P.
 PR ;
 PR 11 APR 2000; 2000US-19600P.
 PR ;
 PR 11 APR 2000; 2000US-19618P.
 PR ;
 PR 11 APR 2000; 2000US-19659P.
 PR ;
 PR 11 APR 2000; 2000US-19820P.
 PR ;
 PR 18 APR 2000; 2000US-19855P.
 PR ;
 PR 25 APR 2000; 2000US-19978P.
 PR ;
 PR 25 APR 2000; 2000US-19955P.
 PR ;
 PR 03 MAY 2000; 2000US-20151P.
 PR ;
 PR 17 MAY 2000; 2000WO-US13705.
 PR ;
 PR 22 MAY 2000; 2000WO-US14042.
 PR ;
 PR 30 MAY 2000; 2000WO-US14941.
 PR ;
 PR 02 JUN 2000; 2000WO-US15126A.
 PR ;
 PR 05 JUN 2000; 2000US-20832P.
 PR ;
 PR 28 JUL 2000; 2000WO-US07101.
 PR ;
 PR 22 AUG 2000; 2000US-0634848.
 PR ;
 PR 08 NOV 2000; 2000WO-US323B.
 PR ;
 PR 01 DEC 2000; 2000WO-US2578.
 PR ;
 PR 20 DEC 2000; 2000WO-US34956.
 PR ;
 PA (GERH) GENENTECH INC.
 XX Baker R P, Chen J, Desnoyers L, Goddard A, Godowski P J, Gurley A L,
 PI Fan J, Smith V, Watanabe C K, Wood M I, Zhang Z;
 XX WPI: 2001-602745/6B.
 DR N-FSDB, RAS15954.
 XX
 PT Novel nucleic acids encoding PRO polypeptides, used to diagnose the
 PT presence of tumours, such as prostate and breast tumours, in mammals and
 PT to screen for modulators of the compounds -
 XX
 PS Claim 11: FIG 80: 774PP: English.
 XX
 OS Homo Sapiens.
 XX
 PN WO200153182-A1.
 XX
 PR 26 JUL 2001.
 XX
 PE 26-DEC-2000; 2000WO-US34263.
 XX
 PE 26-DEC-2000; 2000WO-US34264.
 XX
 PR 21 JAN 2001; 2000US-1488725.
 PR 25 APR 2001; 2000US-0552217.
 PR 09 JUL 2001; 2000US-0598442.
 PR 19 JUL 2001; 2000US-0620112.
 PR 01 AUG 2001; 2000US-065350.
 PR 14 SEP 2001; 2000US-0652191.
 PR 19 OCT 2001; 2000US-0653466.
 PR 29 NOV 2001; 2000US-027344.
 XX
 PA (HVE) HYESU INC.
 XX

QY	251 DGASRYVLYGNGNRGRASRAELRLREPEDPAHKPSPHDLYFEKSPNFTYSSRGTAGT	310	PR	01-SEP-2005; 200005-0249345.
Db	253 DATEVERPREGVGSRA-----IVPRQAQKHTEDMLPSPCDEJMRSVIAI	305	PR	01-SEP-2005; 200005-0229509.
QY	311 ASGRACNNSSPALDCCSGLCGHTRTORVERCNCFTWCCINSRNCGHTRLHEC	369	PR	05-SEP-2005; 200005-0229535.
Db	305 RGRTCNKTSAIDCELLCCRGFTANVELERCSKFWYFVKGRCLVLEHT	364	PR	06-SEP-2005; 200005-0240437.
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ID	AAE09707 standard; Protein; 365 AA.		PR	08-SEP-2005; 200005-0241968.
XX			PR	12-SEP-2005; 200005-0241961.
AAE09707;			PR	12-SEP-2005; 200005-0241968.
XX			PR	14-SEP-2005; 200005-0242397.
DT	22-NOV-2001 (first entry)		PR	14-SEP-2005; 200005-0242398.
VX			PR	14-SEP-2005; 200005-0242399.
JE	Human gene 's encoding novel protein: HMGCR1. Seq ID No.:54.		PR	14-SEP-2005; 200005-0242400.
XX			PR	14-SEP-2005; 200005-0242401.
KW	Human; cytostatic; gene therapy; inflammatory disorder; neural disorder;		PR	14-SEP-2005; 200005-0242403.
KW	Parkinson's disease; Alzheimer's disease; immune system disorder; AIDS;		PR	14-SEP-2005; 200005-0242404.
KW	autoimmune disease; rheumatoid arthritis; muscular disorder; ischaemia;		PR	14-SEP-2005; 200005-0242405.
KW	reproductive disorder; Crohn's disease; pulmonary disorder; cancer;		PR	21-SEP-2005; 200005-0242423.
KW	myocardial infarction; glomerulonephritis; nephrotic syndrome; tumour;		PR	21-SEP-2005; 200005-0242424.
KW	haemopoietic disorder; rhinitis; asthma; diabetes; atherosclerosis;		PR	25-SEP-2005; 200005-0244949.
KW	anti sense therapy; endocrine disorder; leukaemia.		PR	26-SEP-2005; 200005-0245494.
XX			PR	27-SEP-2005; 200005-0245494.
OS	Homo sapiens.		PR	27-SEP-2005; 200005-0245844.
XX			PR	29-SEP-2005; 200005-0246327.
FN	WG200155202_A1.		PR	29-SEP-2005; 200005-0246361.
XX			PR	29-SEP-2005; 200005-0246368.
PD	02-AUG-2001.		PR	29-SEP-2005; 200005-0246369.
XX			PR	29-SEP-2005; 200005-0246370.
PF	17-JAN-2001; 2001WD-US91325.		PR	29-SEP-2005; 200005-0246370.
XX			PR	02-OCT-2005; 200005-0246802.
PR	31-JAN-2000; 200005-0179065.		PR	02-OCT-2005; 200005-0247037.
PR	04-FEB-2000; 200005-0180628.		PR	02-OCT-2005; 200005-0247038.
PR	24-FEB-2000; 200005-0184664.		PR	02-OCT-2005; 200005-0247039.
PR	02-MAR-2000; 200005-0186350.		PR	02-OCT-2005; 200005-0247040.
PR	16-MAR-2000; 200005-0189874.		PR	13-OCT-2005; 200005-0249935.
PR	17-MAR-2000; 200005-0190076.		PR	13-OCT-2005; 200005-0249937.
PR	18-APR-2000; 200005-01918123.		PR	20-OCT-2005; 200005-0240950.
PR	19-MAY-2000; 200005-0205515.		PR	20-OCT-2005; 200005-0241221.
PR	07-JUN-2000; 200005-0209467.		PR	20-OCT-2005; 200005-0241795.
PR	28-JUN-2000; 200005-0214886.		PR	20-OCT-2005; 200005-0241786.
PR	30-JUN-2000; 200005-0215135.		PR	20-OCT-2005; 200005-0241787.
PR	07-JUL-2000; 200005-0215647.		PR	20-OCT-2005; 200005-0241787.
PR	07-JUL-2000; 200005-0216980.		PR	20-OCT-2005; 200005-0241789.
PR	11-JUL-2000; 200005-0217487.		PR	20-OCT-2005; 200005-0241794.
PR	11-JUL-2000; 200005-0217496.		PR	01-NOV-2005; 200005-0244617.
PR	14-AUG-2000; 200005-0218290.		PR	08-NOV-2005; 200005-0246474.
PR	26-JUL-2000; 200005-0220963.		PR	08-NOV-2005; 200005-0241786.
PR	26-JUL-2000; 200005-0220964.		PR	08-NOV-2005; 200005-0241787.
PR	14-AUG-2000; 200005-0224518.		PR	08-NOV-2005; 200005-0241787.
PR	14-AUG-2000; 200005-0224519.		PR	08-NOV-2005; 200005-0241787.
PR	14-AUG-2000; 200005-0225213.		PR	08-NOV-2005; 200005-024523.
PR	14-AUG-2000; 200005-0225214.		PR	08-NOV-2005; 200005-0246524.
PR	14-AUG-2000; 200005-0225265.		PR	08-NOV-2005; 200005-0246525.
PR	14-AUG-2000; 200005-0225267.		PR	08-NOV-2005; 200005-0246526.
PR	14-AUG-2000; 200005-0225270.		PR	08-NOV-2005; 200005-0246477.
PR	14-AUG-2000; 200005-0225447.		PR	08-NOV-2005; 200005-0246478.
PR	14-AUG-2000; 200005-0225757.		PR	08-NOV-2005; 200005-0246478.
PR	14-AUG-2000; 200005-0225758.		PR	08-NOV-2005; 200005-0246478.
PR	14-AUG-2000; 200005-0225759.		PR	08-NOV-2005; 200005-0246478.
PR	18-AUG-2000; 200005-0226279.		PR	08-NOV-2005; 200005-0246478.
PR	22-AUG-2000; 200005-0226581.		PR	08-NOV-2005; 200005-0246478.
PR	22-AUG-2000; 200005-0226868.		PR	08-NOV-2005; 200005-0246478.
PR	23-AUG-2000; 200005-0227009.		PR	08-NOV-2005; 200005-0246478.
PR	30-AUG-2000; 200005-0228924.		PR	08-NOV-2005; 200005-0246478.
PR	01-SEP-2000; 200005-0229287.		PR	08-NOV-2005; 200005-0246478.

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Gencore version 5.1.4-F5-4578

OM protein - protein search, using sw model

Run on: April 22, 2003, 16:38:38 : Search time 36 Seconds
 (without alignments)

362,983 Million cell updates/sec

Title: US-09-674-292-1

Perfect score: 2036

Sequence: I MGLWALFGNVSATLLALA..... WOCHVSGCNCTHRYLHEC1 870

Scoring table: BL0SM6M2

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 9

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Issued Patents_AA: *

- 1: /cqn2-5/ptodata/1/aa/5B/COMB pep: *
- 2: /cqn2-5/ptodata/1/aa/5B/COMB pep: *
- 3: /cqn2-5/ptodata/1/aa/6A/COMB pep: *
- 4: /cqn2-6/ptodata/1/aa/6B/COMB pep: *
- 5: /cqn2-6/ptodata/1/aa/pecnS/COMB pep: *
- 6: /cqn2-6/ptodata/1/aa/backfillseq.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Length	DB ID	Description
1	840.5	41.3	355	3	US-09-082-270-2
2	834	41.0	4	US-09-082-782A-2	
3	756	37.1	357	1	US-09-082-782B-8
4	731.5	35.9	372	3	US-09-082-089A-3
5	723.5	35.5	359	3	US-09-082-089A-5
6	720.5	35.4	363	3	US-09-082-089A-5
7	709.5	34.8	349	4	US-09-459-774-2
8	709.5	34.8	389	2	US-09-485-449-7
9	709.5	34.7	389	2	US-09-485-449-6
10	679	33.3	376	2	US-09-485-449-5
11	373.5	18.3	159	3	US-09-082-170-4
12	336.5	16.5	121	4	US-09-067-782A-5
13	325	11.1	131	4	US-09-067-782A-4
14	113.5	5.6	115	2	US-09-485-449-4
15	99	4.9	1652	4	US-09-485-449A-2
16	99	4.9	956	1	US-09-416-523-2
17	99	4.9	956	3	US-09-789-478-2
18	96	4.7	399	4	US-09-518-869-2
19	96	4.7	399	4	US-09-553-704-7
20	96	4.7	399	4	US-09-518-869-2
21	91	4.4	1652	4	US-09-485-449A-2
22	89.5	4.4	1652	4	US-09-627-550B-2
23	89.5	4.4	1652	4	US-09-436-063C-3
24	89.5	4.4	1917	4	US-09-436-063C-5
25	89.5	4.4	2508	4	US-09-627-550B-7
26	89.5	4.4	2508	4	US-09-436-063C-7
27	89.5	4.4	2508	4	US-09-436-063C-7

ALIGNMENTS

RESULT 1

US-09-082-270-2

Patent No. 6043553

GENERAL INFORMATION:

APPLICANT: BARNES, MICHAEL

APPLICANT: TESTA, TANIA

TITLE OF INVENTION: NO. 6,630,531 Compounds

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: FATHER S. PRESTIA

STREET: P.O. BOX 980

CITY: VALLEY FORGE

STATE: PA

ZIP: 19482

ZIP: 19482

COUNTRY: USA

COMPUTER READABLE FORM:

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FASTSEU for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US-09-082-270-2

FILING DATE: 23-MAY-1998

CATEGORIZATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: SH-3710716-3

FILING DATE: 23-MAY-1999

APPLICATION NUMBER: SH-9904921-6

FILING DATE: 06-MAR-1998

ATTORNEY/AGENT INFORMATION:

NAME: PRESTIA, PAUL F.

REGISTRATION NUMBER: 23,061

REFERENCE/CORRECT NUMBER: SH-30164

TELECOMMUNICATION INFORMATION:

TELEPHONE: 610-417-0705

TELEFAX: 610-417-0702

TELEX: 84165

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 315 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MEDICINE TYPE: protein

US-09-082-270-2

Query Match Best Local Similarity 45.0%; Preceded by 1.4e-77; Matches 155; Conservative 52; Mismatches 12; Indexes 9; Gaps 3;

QY 34 WMSIVNVAASINNLITUSKLWVPEPSQLSKRRLIKNPGLAHVSGALQAVREC 93
Db 26 WMSLALGQVTS----GSUPPLLOGSIRPLVYKQLFCRNTEIMSVSAEVKIGIE 80
QY 94 KNGFRURKWNTPAPGP-HFGKINNGCREPAAFIATAGVHVARSEGGEST 152
Db 81 QHOFRRBRACTTIDUSLAIFGPVLKATRESFVHALASGAVFAIRSAEGSTI 146
QY 153 GGYRRRSPGPDRHWGCSNDNDFGRFLGREFDVSSEKJDRLFMLNHNEAGRTIVES 212
Db 141 CDSHHKPGPSEGKWWGCCSDADFOVLYSREFADARENTRARSAMKHNEAGTTI 200
QY 213 EMRQECKHMGSCUTFTCWRKLTIAVGDKLRFED-AASRLYNGNSKRAEEL 272
Db 201 HMLIKKCHLSSCEVKTOMAQDFRAGHLERLKQVYSAENW--EHRSREWVE 257
QY 273 RLEPEPAHKPSPSHLUVYERKSPNCTYSGHTGATGACSSPAECC 332
Db 258 TLRKAYSLSKPPERDLYVYENSPCEPENPTEGSRTRCTWNTSGIQCCLGCR 317
QY 333 GHTRKQVRCHNTHCWHCNSCRNTHRYLHE 369
QY 318 GHNTREKEKKEKCIIHWCQVNSQECIRIVHIC 354

RESULT 2
US-09-067-782A-2
Sequence 2, Application US/J0936782A
; Patent No. 6165751
GENERAL INFORMATION:
APPLICANT: BARNES, MICHAEL
TITLE OF INVENTION: NOVEL COMPOUNDS
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Partner & Prestia
STREET: P.O. Box 969
CITY: Valley Forge
STATE: PA
COUNTRY: US
ZIP: 19482-0969
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US09/067-782A
FILING DATE: 28-APR-1998
CLASSIFICATION: 435
PRIORITY APPLICATION:
APPLICATION NUMBER: UK 9710734-6
FILING DATE: 23-MAY-1997
APPLICATION NUMBER: EP 97309144-0
FILING DATE: 12-NOV-1998
ATTORNEY/AGENT INFORMATION:
NAME: Preslia, Paul F
REGISTRATION NUMBER: 23,031
REFERENCE/DOCKET NUMBER: GH-30167
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-407-0700
TELEX: 846169
TELEFAX: 610-407-6761
SEQUENCE CHARACTERISTICS:
LENGTH: 351 amino acids
TYPE: amino acid
STRANGENESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
; US-09-067-782A-2

RESULT 3
US-09-067-928-8
Sequence 8, Application US/09647928
; Patent No. 578291
GENERAL INFORMATION:
APPLICANT: Roman, Gideon A.
TITLE OF INVENTION: DNA ENCODING THE WNT-X GROWTH FACTOR
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: John W. Waijen
STREET: 126 E. Lincoln Avenue
CITY: Rahway
STATE: New Jersey
COUNTRY: USA
ZIP: 07065
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.2;
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/067-928
FILING DATE: 22-MAR-1996
CLASSIFICATION: 435
PRIORITY APPLICATION:
APPLICATION NUMBER: 08/172,365
FILING DATE: 22-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Waijen, John W.
REGISTRATION NUMBER: 35,453
REFERENCE/DOCKET NUMBER: 19416
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-3905
TELEFAX: (908) 594-4720
SEQUENCE CHARACTERISTICS:
LENGTH: 397 amino acids
TYPE: amino acid
STRANGENESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
; US-09-067-928-8

Matches Local Similarity 44.6% Pred. No. 6,3e-124; Iter. S 20; Gaps 14 TLLLAALAFALLANSSGRGWGIVNVASSINNLITUSKLWVPEPSQLSKRRLIKNPGLAHVSGALQAVREC 93
QY 9 STLLVYFAVEASAAN----WLYLAKLSSVGSISSEETCE---EKKI-TORQWLMCK 58
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QY 134 GYTHSWARSEESIESTYMRRQGPSPDHM3GCSNDPDKHJGKPFHFSFVUGERK- 192
Db 119 QYAFAVTRACSSGLEK-SGCTYHGVSPOGFOWSGCNSUNAIVAS-SFVWRESK 178
QY 193 -DLRFTEAHNNFAGRITIVSEMEQKCHRSQGSCUTTOMBRHJLPAFVGWVDRF 250
Db 179 ASSRADMHNHNGRAKALTHMAYEKCHOBVSECEVKCKAVI-EFVSHAIKE 238
QY 251 TGSASRVLIYRGNSNRAEELRLEPEPAHKPSPHFLDVYEFKSYCNGSFRGAT 310
Db 239 LDATEVEFPGVSE-----LYPRNAQKPHTDDEWYLEPST-PCLOMSQVGT 291
QY 311 ASFACNSHSSLADORELJPGFERTGFRHTFTRVTERCZHWHCVHS-S-THTRVHLIC 369
Db 292 KSRTCNKTSAKLDGCELLSOSRGFMIAQVLAERGSCSKHWCVEK-PC-REVELHIC 350

FILING DATE: 25-FEB-1998
 APPLICATION NUMBER: GB 9804007.4
 FILING DATE: 25-FEB-1998
 ATTORNEY/AGENT INFORMATION:
 NAME: PRESTIA, PAUL F.
 REGISTRATION NUMBER: 21,031
 REFERENCE/DOCKET NUMBER: GH-30166
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 610-407-0700
 TELEX: 846169
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 359 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-09-002-089-3

Query Match 35.5%; Score 723.5; DB 3; Length 359;
 Best Local Similarity 39.0%; Pred No. 1-2e-65; Mismatches 7;
 Matches 142; Conservative 65; MisMatches 22; Indels 35; Gaps 7;

QY 15 ULLAALAPRALA---ANSGRGMWIVNVAASITLITUSKSLQVLEP---SOLLSR 66
 Db 5 ILLFLAALISSLWAQLTIDANS---KWSL---ALNWVPEMFTIGAQPVSLPLGLSF 56

QY 67 KURRLRQPGHISVGGLGOSAVECKWOFNRNRNGPAPPHLAKINRATF 26
 Db 57 GORKLCQLQEHMAYREGAKTGIRECONQFOPRFKOSTANASVERWQWISRETAF 116

QY 127 LFATISAGYTHVARSESEGSESTCYYPRGPSSKHWACSENLLPKFGEV 185

Db 117 THAVSAGVYNASRASEGSESTGCRTRKULFQWKLWQGNEVYHRAKEV 176

QY 186 DSIEKGEL-----REFNMHNNEAERTVSEMPKJHMSSDUTVTPMLP 237

Db 177 DARERENKTAKGSEEUGRMVNQNNEARAVKAWADAKTHGVRSCKTLWLA 236

QY 238 TIRAVEDWVDRDEGASVLYGNRNSRASRABLLMEPEPAHKPSPHLVEKFN 297

Db 237 EFRKVGDALKERKUASAMVRK-----RLELVNSRTOPTIVEDWYDFSD 286

QY 298 FCTYSRSLGIFTAGRACNNSSPADGELLLUCGHRHTPQTQTERNCFHWCHS 157

Db 287 VCLRNSTGSGIUGRLONKTSEMGDCHELMGCGYQYNGKSVWERKCHERHWFCKC 416

QY 358 RKC1 351

347 KKCT 355

RESULT 6

US-09-002-089-5
 Sequence 5, Application US-09082089
 Patent No. 6,200,650
 GENERAL INFORMATION:
 APPLICANT: BARNES, MICHAEL
 APPLICANT: TESTA, TANIA
 APPLICANT: KESSEL, DAVID
 TITLE OF INVENTION: Novel Combinations
 NUMBER OF SEQUENCES: 5
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: RATHER & PRESTIA
 STREET: P.O. BOX 940
 CITY: VALLEY FORGE
 STATE: PA
 COUNTRY: USA
 ZIP: 19482
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM compatible

OPERATING SYSTEM: DOS
 SOFTWARE: FASTA for Windows Version 2.0
 CURRENT APPLICATION DATA: US-09-002-089
 PATENT NUMBER: 6,200,650
 FILING DATE: 20-MAY-1998
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 38 993 544-7-4
 FILING DATE: 25-FEB-1998
 ATTORNEY/AGENT INFORMATION:
 NAME: PRESTIA, PAUL F.
 REGISTRATION NUMBER: 21,031
 REFERENCE/DOCKET NUMBER: GH-30166
 TELEPHONE: 610-407-0700
 TELEX: 846169
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 463 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-09-002-089-5

Query Match 35.5%; Score 723.5; DB 3; Length 359;
 Best Local Similarity 39.0%; Pred No. 1-2e-65; Mismatches 7;
 Matches 142; Conservative 65; MisMatches 22; Indels 35; Gaps 7;

QY 15 ULLAALAPRALA---ANSGRGMWIVNVAASITLITUSKSLQVLEP---SOLLSR 66
 Db 5 ILLFLAALISSLWAQLTIDANS---KWSL---ALNWVPEMFTIGAQPVSLPLGLSF 56

QY 67 KURRLRQPGHISVGGLGOSAVECKWOFNRNRNGPAPPHLAKINRATF 26
 Db 57 GORKLCQLQEHMAYREGAKTGIRECONQFOPRFKOSTANASVERWQWISRETAF 116

QY 127 LFATISAGYTHVARSESEGSESTCYYPRGPSSKHWACSENLLPKFGEV 185

Db 117 THAVSAGVYNASRASEGSESTGCRTRKULFQWKLWQGNEVYHRAKEV 176

QY 186 DSIEKGEL-----REFNMHNNEAERTVSEMPKJHMSSDUTVTPMLP 237

Db 177 DARERENKTAKGSEEUGRMVNQNNEARAVKAWADAKTHGVRSCKTLWLA 236

QY 238 TIRAVEDWVDRDEGASVLYGNRNSRASRABLLMEPEPAHKPSPHLVEKFN 297

Db 237 EFRKVGDALKERKUASAMVRK-----RLELVNSRTOPTIVEDWYDFSD 286

QY 298 FCTYSRSLGIFTAGRACNNSSPADGELLLUCGHRHTPQTQTERNCFHWCHS 157

Db 287 VCLRNSTGSGIUGRLONKTSEMGDCHELMGCGYQYNGKSVWERKCHERHWFCKC 416

QY 358 RKC1 351

347 KKCT 355

RESULT 7

US-09-002-089-5
 Sequence 2, Application US-09082089
 Patent No. 6,200,650
 GENERAL INFORMATION:
 APPLICANT: Michael Robert Barnes
 APPLICANT: Tania Tanson Testa
 TITLE OF INVENTION: Novel Combinations
 FILE REFERENCE: SP-30193
 CURRENT APPLICATION NUMBER: US-09-002-089-7-4

TELEPHONE: (415) 813-5600
 TELEFAX: (415) 494-0792
 TELEX: 706141
 INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 389 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLGY: linear

US-08-485-449-7

Query Match 34.8%; Score 709.5; DB 2; length 389;
 Best Local Similarity 38.5%; Pred. No. 3; e-64; Mismatches 10; Gaps 10;
 Matches 153; Conservative 53; MisMatches 122; Indels 59; Gaps 10;

QY 23 PAALANANSRGRGWINVVAASSTNLTS-KSLOVLER-----SLLSLSKORLLI 72
 Db 11 PSGLA-----GLFLAKCSKALSNELISLKLGEFFPLNTVLTLSGSKROLGC 62
 QY 73 RNPEDVITVSGLGLOAVRECKNQFRHMRNPPIAH-----PHLEKIVNGRETAVL 128
 Db 63 LRNPDVITVSALOGHLTAHVBCQHQLQRWNSALEGGGRPH-HAILKRFESAFSE 121
 D 129 AITSAGVHVSVARSESEGSEESTCDHRG-----KRSKHS 159
 Db 122 SMLAAGVHMAVATCALKVSKVSGCGKSEQLIBAKLQLQALSRGKSFPSLSPG 181
 QY 160 -----P33CWHMWSUNIKDGRGREGRENSERTRALSFMLHNNEATIVES 212
 Db 182 PGSPSPGPJUTNEWGJONHUMGFERPSRDFDSKAEPDIAURHINRNGROVTE 241
 QY 213 EMWECCKHMSASCVTWRBLTFPAWNVNHFEGASAVVGNFSSNAEFL 272
 Db 242 NLIKCKCRHTJSOFCOKTOWRAPEFRAVGAALRRL--SRAFIIDH-BHNSGAKU 297
 QY 273 RLFEDPAPKPPSPHDLVFEKSFNFETISGLTAGTAAAGRA'NSSPALDGELLCCR 332
 Db 298 RLRRPLS-----SELVYFEKSPDCEPDTMSPGSPTRGRANKTSRLIGGSLCCR 351
 QY 333 GHRTETQWTERNCFHWCHASCRNCTRVIHEC 369
 Db 352 GHNVLROTRVERCHCROHPCOVCYLCDECKVTEWNV 383
 Db

RESULT 10

US-08-485-449-6

Sequence 6: Application US/08485449

Patent No. 5824789

GENERAL INFORMATION:

APPLICANT: VANDENBERG, DAVID

TITLE OF INVENTION: HEMATOPOIETIC GROWTH FACTORS, NUCLEOTIDE

TITLE OF INVENTION: SEQUENCE ENCODING GROWTH FACTORS AND METHODS OF USE

NUMBER OF SEQUENCES: 7

CORRESPONDENCE ADDRESS:

MORRISON & FOSTER

STREET: 755 Page Mill Road

CITY: Palo Alto

STATE: California

ZIP: 94304-1108

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.40

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/485,449

FILING DATE:

CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:

NAME: KONSKI, ANTOINETTE F.

REGISTRATION NUMBER: 34,202

REFERENCE/OCKET NUMBER: 20296-20035.00
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 813-5600
 TELEFAX: (415) 494-0792
 TELEX: 706141
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 389 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLGY: linear

US-08-485-449-6

Query Match 34.7%; Score 707; DB 2; length 389;
 Best Local Similarity 39.5%; Pred. No. 6.6e-64; Mismatches 119; Indels 60; Gaps 8;

Matches 149; Conservative 48; MisMatches 119; Indels 60; Gaps 8;

QY 43 STNLITSKSLQVLP-----SLLSLSKORLLI 72
 Db 24 SRLSNELGKLGKPEPLNTVLTLSGSKRGUDRSFVIMASQHAYHEC 83
 QY 94 KWOENP-SANCPTAG---PHFSKVNRFSTETAFITA-NWBSVARSSESE 149
 Db 84 QHOLQHFRNCSCLES33R-LH-BSAIIKRFERESAESFMSLA-WBAYATASLKV 142
 QY 150 SCLTYRFGS-----P33CWHMWSUNIKDGRGREGRENSERTRALSFMLHNNEATIVES 212
 Db 14 SOSCKRJS3EGRKAKLQJALSRSKIPP:SUSPVPGSVFSPG-LTWNG3NHD 202
 QY 174 TDFGRFREFWNGEKGHRMFLNMNNEAGRTVSEMOKR-BMSGSVWTW 233
 Db 245 KOGKESDESLRSERASRFAVMMRHNWVAVVNEVNNERK-RK-BTSQWPKCW 252
 QY 234 MRPILKAVGDUKJFGDGSRKLWNGRGSNRSAEELRPE-PAKKEFPHLYFE 293
 Db 263 RAPEFRA-GAHLRRL--SRAFIIDH-BHNSGAEFQPRPRLS-----GELVYFE 312
 QY 294 KSPNQTCISGRGTATZAGAACSSSALLACECCGSRGHTRKTC-ERGCFIWCC 353
 Db 313 KSPDFOERDPTLSPGTRGACKNTSRLLQGSCCGHRYVLSKOTEVERCHOREHWCC 372
 QY 354 HWSCTGTRHLHEC 369
 Db 473 YVLCDECKTYEVNVC 388
 Db

RESULT 11

US-08-485-449-5

Sequence 5: Application US/08485449

Patent No. 5824789

GENERAL INFORMATION:

APPLICANT: VANDENBERG, DAVID

TITLE OF INVENTION: HEMATOPOIETIC GROWTH FACTORS, NUCLEOTIDE

TITLE OF INVENTION: SEQUENCE ENCODING GROWTH FACTORS AND METHODS OF USE

NUMBER OF SEQUENCES: 7

CORRESPONDENCE ADDRESS:

MORRISON & FOSTER

STREET: 755 Page Mill Road

CITY: Palo Alto

STATE: California

ZIP: 94304-1108

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/485,449

FILING DATE:

CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:

NAME: KONSKI, ANTOINETTE F.

REGISTRATION NUMBER: 34,202

NAME: KONSKI, ANTOINETTE F.
 REGISTRATION NUMBER: 34,202
 REFERENCE/DOCKET NUMBER: 20295-20035.00
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 813-5000
 TELEX: 70641
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 376 amino acids
 STRANDEDNESS: Single
 TOPOLOGY: Linear
 US-08-485-449-5

Query Match 33.3%; Score 679; DB 2; Length 376;
 Best Local Similarity 39.5%; Pred No. 4 5e-61; Mismatches 11;
 Matches 149; Conservative 49; Gaps 58; Gaps 11;

QY 36 GIVNVAASTMLTDSKTSQVLEP----SLLSLRSQRRLRIRQNLPGILHSVSGNQ 87
 Db 14 GLFLALSRASLNLKPLKPGEPPLNTVCLSLQGICLR-PDVTAQSLH 72

QY 88 SAVRECKWQERNRWNKPTAPG---PHIFGKVNGCGRATEFFATTSAGTHVSAACT 143
 Db 73 IAVHECOHQDQRDWNSALEBGGGLPH-H-SATLTKRGFRESAFSFSMLAGYMHAVATC 131

QY 144 SEGSISCTSDYRRG-----PGPD----WHWGCD 172

Db 132 SLGKLVSGCGWKGSGCDRLAKLQLQALSRAKPSPPSPSPFGPDTWEGGNH 191

QY 173 NTOFGRLFGFPEVPSGKDRFLMLNNNEAGRIVTFSEMOECKCHGMMSGCTVR 212
 Db 192 DMDGFKEFSDFLSRSEAPDIOQAMRNTRUNNRGRQWVTEKLKCKKGSGSQEKIC 251

QY 233 WMRPLTPURAYGVDFRDGASRVYNGNSNAAASRLEREDPAKKPSPHOLVFE 292
 Db 252 WRAPERAAQALRRL---RAFELI-HNNSAFAQFLRRLS----SELVYF 295

QY 293 EKPNFTYSGRLTAGRACNESSPAIDGEELLOGRHRHTQUTTERCNCFHW 352

Db 300 EKSPDFEE-RDPTGSPGIRGRACKNTSRLIGGSLOCGRHNVLKTRVERCHRFH 358

QY 353 CHVSNCNTHTRVHEC 369

Db 359 CIVLDECKTIEWVMC 375

RESULT 12
 US-08-270-4

Sequence 4 Application US/09082270
 Patent No. 6044053

GENERAL INFORMATION:

APPLICANT: BARRES, MICHAEL
 TITLE OF INVENTION: NO. 6043053el Compounds
 NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:
 ADDRESSEE: RATER & PRESTIA
 STREET: P.O. BOX 980
 CITY: VALLEY FORCE
 STATE: WA
 COUNTRY: USA

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FASTSEU for Windows Version 2.0

APPLICATION DATA:
 APPLICATION NUMBER: US/09/082270
 FILING DATE: 28 APR 1998
 CLASSIFICATION: 435

PRI-1 APPLICATION DATA:
 APPLICATION NUMBER: UK 9710734.6
 FILING DATE: 23 MAY 1997
 APPLICATION NUMBER: EP 97309144.0
 FILING DATE: 13-N-V-1998
 ATTORNEY/AGENT INFORMATION:
 NAME: Prestia, Paul F.
 REGISTRATION NUMBER: 23,031
 REFERENCE/DOCKET NUMBER: GH-30164
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 610-407-0700
 TELEX: 64519
 FAX: 610-407-0701

SEQUENCE CHARACTERISTICS:
 LENGTH: 159 amino acids
 TYPE: amino acid
 STRANDEDNESS: Single
 TOPOLOGY: Linear
 MOLECULE TYPE: Protein
 US-09-082-270-4

Query Match 39.3%; Score 373.5; DB 2; Length 159;
 Best Local Similarity 49.0%; Pred No. 2 1e-33; Mismatches 11;
 Matches 171; Conservative 19; Gaps 5; Gaps 1;

QY 105 TAPGHLEGKVNRLQIPTATAFATTSAVTHVARCSEGSEGSIESCIQYRKGPGPDM 165
 Db 8 SVBETL-----NATPESAVTHASAVAFATVPSAEISI-GPSDHKKGPGESW 62

QY 255 HWHE-SUNIFGRLGSEPVSGKDRFLMLNNNEAGRIVTFSEMOECKCHGMMSG 225
 Db 63 KW3Q5EDADFGVLUFGYDAKENFDARSAMKHNNEA-KTTLQHMHKQFHGLG 122

QY 226 SCHVTCOMRPIKTVAVMURFUGA 253
 Db 123 SPVKICWAWLFAIUDFKUKYUSA 156

RESULT 13
 US-09-067-782A 5

Sequence 5 Application US/09067782A
 Patent No. 6107551

GENERAL INFORMATION:

APPLICANT: BARNES, MICHAEL
 TITLE OF INVENTION: N-Acetyl-M-mannosyl
 NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Rater & Prestia
 STREET: P.O. Box 980
 CITY: Valley Force
 STATE: WA
 COUNTRY: US

ZINC: 1342-6690

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FASTSEU for Windows Version 2.0

APPLICATION DATA:
 APPLICATION NUMBER: US/09/082270
 FILING DATE: 28 APR 1998
 CLASSIFICATION: 435

PRI-1 APPLICATION DATA:
 APPLICATION NUMBER: UK 9710734.6
 FILING DATE: 23 MAY 1997
 APPLICATION NUMBER: EP 97309144.0
 FILING DATE: 13-N-V-1998
 ATTORNEY/AGENT INFORMATION:
 NAME: Prestia, Paul F.
 REGISTRATION NUMBER: 23,031
 REFERENCE/DOCKET NUMBER: GH-30164
 TELECOMMUNICATION INFORMATION:

US-09-067-782A-4

Query Match 11.1%; Score 225; DB 4; Length 131;
Best Local Similarity 36.8%; Pred. No. 2.3e-15;
Matches 49; Conservative 32; Mismatches 42; Jt.Jets 10; Gaps 2;

QY 14 TELLALAPALAAANSKRWGIVNVASSNLTSKLQLVPEPSLJSRQRLL 73
Db 4 SRLVFAFSAASN---WILAKLSSGSISSECE..EKLILKQVNCCK 56

27 74 UNPGILHSUSSGJOSAVKEKWJERNPWNCPAPSAPHGKVNKTETATIFATSA 134
Db 59 ENLEMUSPHRAQALETCYEFKRNHNSLTSLWKNV..SILARVIASSA 118

QY 134 SYTHVARSCSIS 146
Db 119 CWGEFAVTACNS 131

RESULT 15 US-09-067-782A-4

Sequence 4, Application US/08485449
; Patent No. 5824399

GENERAL INFORMATION:
APPLICANT: BARNES, MICHAEL
TITLE OF INVENTION: NOVEL COMPOUNDS
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Barnes & Prestia
STREET: P.O. Box 980
CITY: Valley Forge
STATE: PA
COUNTRY: US
ZIP: 19482-0980

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FIRSTSEL for Windows Version 2.0

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/067-782A
FILING DATE: 28-APR-1998
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 9710734.6
FILING DATE: 23-MAY-1997
APPLICATION NUMBER: EP 97309144.0
FILING DATE: 13-NOV-1998
ATTORNEY/AGENT INFORMATION:
NAME: Prestia, Paul F
REGISTRATION NUMBER: 23-031
REFERENCE/DOCKET NUMBER: 430167

TELECOMMUNICATION INFORMATION:
TELEPHONE: 601-407-0700
TELEFAX: 601-407-0701
TELEX: 846169

INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 131 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein

Query Match 5.5%; score 113.5; DB 2; Length 115;
Best Local Similarity 32.1%; Pred. No. 0.00045;
Matches 36; Conservative 17; Mismatches 36; Jt.Jets 23; Gaps 5;

QY 23 PAALANSSGGWGVNVASNLTLTSKSLQVLEH----SILLSRQRLL 72
Db 11 PSGLA-----GELFLAGCRALSNETLGKLPSPPLTGNTVCLLSISKQGLC 62

QY 73 RQNGIILHSVGGLOSSAVERKWQFNPRNCITAPS---PHIFSKVNG 120
Db 63 LRNPDPVITASALQGLIAVHECQHQLRQRCNCSALEGGGRPH-HSAIKS 113

Wed Apr 23 07:41:00 2003

us-09-674-292-1.rai

Page 9

Search completed: April 22, 2003, 16:42:57
Job time : 37 secs

genCore version 5.1_4-p5-4578
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OM protein - protein search, using sw mode.
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 Scoring table: RIGSUM62
 GapP 10.0 , GapExt 0.5
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 Total number of hits satisfying chosen parameters: 3<1>32
 Minimum DB seq length: 0
 Maximum DB seq length: 200000000
 Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database :

Published Applications AA:*

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- 2: /cgns2_6/podata/1/pubpaas/PC1_NEW_PUB_pep:*
- 3: /cgns2_6/podata/1/pubpaas/US06_NEW_PUB_pep:*
- 4: /cgns2_6/podata/1/pubpaas/US07_NEW_PUB_pep:*
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- 9: /cgns2_6/podata/1/pubpaas/US09_PUBCOMB_pep:*
- 10: /cgns2_6/podata/1/pubpaas/US10_NEW_PUB_pep:*
- 11: /cgns2_6/podata/1/pubpaas/US10_PUBCOMB_pep:*
- 12: /cgns2_6/podata/1/pubpaas/US10_PUBCOMB_pep:*
- 13: /cgns2_6/podata/1/pubpaas/US50_NEW_PUB_pep:*
- 14: /cgns2_6/podata/1/pubpaas/US60_PUBCOMB_pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	840	41.3	351 9 US-09-978-295A-225	Sequence 245, APP
2	840	41.3	351 9 US-09-978-659-225	Sequence 225, APP
3	840	41.3	351 9 US-09-978-19A-226	Sequence 226, APP
4	840	41.3	351 9 US-09-83A-226	APPLICANT: Roy, Margaret Ann
5	840	41.3	351 9 US-09-978-189-226	Sequence 226, APP
6	840	41.3	351 9 US-10-174-590-80	Sequence 80, APP
7	840	41.3	351 9 US-10-176-757-80	APPLICANT: Thomas, Jamie
8	840	41.3	351 9 US-10-175-737-80	APPLICANT: Williams, P. Mickey
9	840	41.3	351 9 US-10-173-706-80	APPLICANT: Wood, William L.
10	840	41.3	351 9 US-10-180-557-80	Sequence 80, APP
11	840	41.3	351 9 US-10-175-757-80	TITLE OF INVENTION: Secreted and transmembrane Peptides and Nucleic
12	840	41.3	351 9 US-10-176-482-80	FILE REFERENCE: 026301C1
13	840	41.3	351 9 US-10-176-757-80	CURRENT APPLICATION NUMBER: US10/978-235A
14	840	41.3	351 9 US-10-176-913-80	CURRENT FILING DATE: 2001-10-15
15	840	41.3	351 9 US-10-173-706-80	PRIOR APPLICATION NUMBER: 599719-85
16	840	41.3	351 9 US-10-180-557-80	PRIOR FILING DATE: 2001-07-30
17	840	41.3	351 9 US-10-173-700-80	PRIOR APPLICATION NUMBER: 630762-50
18	840	41.3	351 9 US-10-174-572-80	PRIOR FILING DATE: 1997-10-17
19	840	41.3	351 9 US-10-174-579-80	PRIOR APPLICATION NUMBER: 600964-49

ALIGNMENTS

RESULT 1
 05-09-978-295A-225
 Sequence 245, Application US-09-978-295A
 Patent No. 200115676A1
 GENERAL INFORMATION:
 APPLICANT: Aslakelazi, Avi
 APPLICANT: Baker, Kevin P.
 APPLICANT: Rosestein, David
 APPLICANT: Lesmeyers, Joc
 APPLICANT: Factor, Dan
 APPLICANT: Ferrara, Napoleon
 APPLICANT: Filvaroff, Ellen
 APPLICANT: Gao, Wei-Qiang
 APPLICANT: Hong, Sherman
 APPLICANT: Jeritzen, Mary E.
 APPLICANT: Jorgenson, Paul J. Christopher
 APPLICANT: Prinandi, J. Christopher
 APPLICANT: Shulman, Austin L.
 APPLICANT: Klibavin, Konstantin J.
 APPLICANT: Klibavin, Yury J.
 APPLICANT: Nafir, Mary A.
 APPLICANT: Pan, James
 APPLICANT: Faoni, Nicholas F.
 APPLICANT: Roy, Margaret Ann
 APPLICANT: Shelton, David L.
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Thomas, Jamie

PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085700
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085689
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085580
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085573
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 41.3%; Score 840; DR 9; Length 351;
Best Local Similarity 44.8%; Pred. No. 1.1e+9; Gaps 4;
Matches 161; Conservative 55; Mismatches 123; Indices 20; Gaps 4;

Qy 14 TULLAAALAAALAAANSRGWGVNVAASTNLTSKSQLVLEPSQLLSRKQRLLH 73
Db 9 SIRLYLFAVVAASAN----WLYIAKLSVGSISBETEE----KKGILQYQWMK 58

Qy 74 QNPGLIHSVSGLOSSAVRECKQFNRRNRCPPAPGPHFKTIVNRGGRRFAFITSK 133
Db 59 RNLLEVMSVRSVRAQATIPECQYQFRNRNCSTLSPVFGKVUTGIREAAFYVISA 118

Qy 134 GYTHSWARSESEGIESCTCYRPGPQFDWMMG3SDNDIFGRFLREFUDSGKGR 192
Db 119 GVAFAVIYTRASSGGEKCGCDTIVHQSGFCDFQWSGSCDSNTAYSVAFSQSFYDVERSK 178

Qy 193 --DLRFLMNHNEAGRTVSEMPRECKHGMSGSTVRCWRMLPLRAGDVDRF 250

Db 179 ASSRALMNLINNEAAGRKAITHMRVECKHGVSCEVKTWKAVPERVGHALKF 238

Qy 251 DGSRVVYNGRGSNRASRAELRLEDPAHKPKSPHDLYFERSPNPCITYSRLGTAGC 310
Db 239 DGATEVPRPVQSSA-----LVPRNAQFKPTDDEULVLEPSDFCEQOMRSGVLIT 291

Qy 311 AGRACNSSSPADGCELLOCGCCGHRPRTQRTVRCTHQCCHWSRCRNTHVILHE 369
Db 292 RGRTCNKTSKAIDSCCLLCCGRCGHTAQYELAERCSCKFHCCFVCKRCQCQTLVHLTC 350

RESULT 2
'US-09-674-292-226
Sequence 226, Application US/09978697
; Patent No. US20020165984A1
; GENERAL INFORMATION
; APPLICANT: Asikenazi, Avi
; APPLICANT: Baker, Kevin P.
; APPLICANT: Borstein, David
; APPLICANT: Destroyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Garritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kjavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Teoni, Nicholas F.
; APPLICANT: Toy, Margaret Ann
; APPLICANT: Shelson, David L.
; APPLICANT: Stewart, Timothy A.

; APPLICANT: Imanas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and transmembrane Peptides and Nucleic
; FILE REFERENCE: P26301C27
; CURRENT FILING NUMBER: US/09-6978-697
; CURRENT FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 09/918585.
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/0664249
; PRIOR FILING DATE: 1997-11-03
; PRIOR APPLICATION NUMBER: 60/0665311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/0665364
; PRIOR FILING DATE: 1997-11-27
; PRIOR APPLICATION NUMBER: 60/0677450
; PRIOR FILING DATE: 1998-03-10
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; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/0779470

APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Grimaldi, J. Christopher
 APPLICANT: Gurney, Austin L.
 APPLICANT: Hillian, Kenneth J.
 APPLICANT: Kjavin, Ivar J.
 APPLICANT: Kuo, Sophia S.
 APPLICANT: Napier, Mary A.
 APPLICANT: Pan, James;
 APPLICANT: Paon, Nicholas F.
 APPLICANT: Roy, Margaret Ann
 APPLICANT: Shelton, David L.
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tums, Daniel
 APPLICANT: Williams, P. Mickey
 TITLE OF INVENTION: Secreted and transmembrane Polypeptides and Nucleic
 FILE REFERENCE: P2531PC9
 CURRENT APPLICATION NUMBER: US/19-1978.192A
 CURRENT FILING DATE: 2001-10-15
 PRIOR APPLICATION NUMBER: 09/915585
 PRIOR FILING DATE: 2001-07-30
 PRIOR APPLICATION NUMBER: 60/062250
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; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 41 3%; Score 840; DB 9; Length 351;
; Best Local Similarity 44 8%; Pred. No. 1; le-69;
; Matches 161; Conservative 55; Mismatches 123; Indels 20; Gaps 4;

QY 14 TILLALALPALAANNSGRWAVNVAASNLTDSSKILALELLOLSRKRPLR 73
; Db 9 SIRKILVFAVEASAAN--WLYAKLSSVGSIEETCH---KLKGIGROVOMCK 58

QY 74 QNPGLHVSQIQLAVRECKWPNRWRNAPTAGPHPLVNWIGETATPATSA 136
; Db 59 RNLLEVMSVRGAUAIETECOYUPNRWNSTSDLSPLVFKVUTSTREAAVYISSA 118

QY 134 GVTHSVARSGSBSBSCDUFYRPGGGPFWHGGCSNTUJGFLGREFSEGEKGR 192
; Db 219 GYAVATRAGSSELECCOYVHVSPPAFQSGCINTAVWAPSFVWRPSKG 178

QY 193 -DIFLUMLNEAFTTVEPMRCECKGMGCVTEWMEPLRAVWIVRF 253
; Db 179 ASSPHAMMHNNEAKRLTHMPVERCHGVSSCERYKWHAVFPPQVHALKEF 259

QY 292 FORTNITSKATIGELLOSGEHTAQVELABCSEKIRVSKHODCORVELHIC 369

Db 239 DATEFVEFRVGSSA-----VPRNAKFPHTDOLWVYFPEFEOMRSVGT 291

QY 311 AGRA:NGSSSFALOSSLLCGSHRTQEVTRCNTHW"VHSJNTHTHIVHEC 365

Db 119 GYAFAVTAKASSGELEGGKRVHVSPOGLWGSNDAYWAFSQSMVWRSKG 178

Db 9 SRLLVFAVSAASNN--WLYAKLSSVGSIEETCH---KLKGIGROVOMCK 58

QY 74 QNPGLHVSQIQLAVRECKWPNRWRNAPTAGPHPLVNWIGETATPATSA 136

Db 59 RNLLEVMSVRGAUAIETECOYUPNRWNSTSDLSPLVFKVUTSTREAAVYISSA 118

Db 179 ASSPHAMMHNNEAKRLTHMPVERCHGVSSCERYKWHAVFPPQVHALKEF 259

RESULT 7
 US-10-176-758-80
 ; Sequence 80, Application US/10176758
 ; Publication No. US2003008353A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Chen, Jian
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Goddard, Andre
 ; APPLICANT: Godkewski, Paul J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Pan, James
 ; APPLICANT: Smith, Victoria
 ; APPLICANT: Watada, Colin K.
 ; APPLICANT: Wood, William I.
 ; APPLICANT: Zhang, Zemin
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING THE SAME
 FILE REFERENCE: P3410RC104
 CURRENT APPLICATION NUMBER: US/10/176,758
 CURRENT FILING DATE: 2002-06-21
 Prior Application removed - See File Wrapper or Palm
 NUMBER OF SEQ ID NOS: 612
 SEQ ID NO 80
 LENGTH: 351
 TYPE: PRT
 ; ORGANISM: Homo sapien
 ; US-10-176-758-80
 Query Match 41.3%; Score 840; UB 47; Length: 351;
 Best Local Similarity 44.8%; Pred. No. 1..le-69; Mismatches 161; Indels 20; Gaps 4;
 Matches 161; Conservative 51; Mismatches 123; UB 47; Length: 351;
 QY 14 TULLALAAFLAANNSGGAGVIVNVAASSTNLITDSKSQLVLEFSQIILSRQRMLR 73
 Db 9 SURLLYFAVSSAASN---WLYKLAKLSSVSISEEICE---KLKGGLQVQACK 58
 QY 74 QNPGLHISNGGQSAYEKKWQKWNKNNPAPKOPHFGKVNJ'PAFFAFTA 133
 Db 59 RNLLEMVSYVRGAGLAEEPOYOFRNKWNGSTLSLPVFGKVZQSHAAFYVIASSA 118
 QY 134 GTHSWAVSKSSESIESCIPERKRGPGSPDWHWGSCSNIFPGKAKPEFVDSGEKR- 192
 Db 119 GVAFAVTRATSSGEGLEKCGTGHGVPSQFOQWGSNDIAYGVAFSISFVUVERSK 178
 QY 253 -DLRFLMHNNEAHTITSEMVOKRKHMSCTVTCMRLKTAANGVLRKT 250
 Db 179 ASSHLMNHNNBAGKAIIHLTMVECKHGVSCEVKTCWAVYKPKVGHALKKE 238
 QY 251 EGASKVLYSKRGNKASRAELKEPEPNKPKPSFHULMVEKSTAEISGKTAGT 310
 Db 239 DATEVERFVSSA-----LVPNAVQKPHDEOLVLEPSDFCQDMRSVGLT 291
 QY 311 AGRACNSHAIIDGCELLNGRRGHRTRQRTENCFHWCHVIS'NTHTWLHC 369
 Db 292 KGRTCNKSKAIDGCELLCGGRGHTAALVAFERSCKHWOCFVKPLQURVELHC 350
 119 GVAFAVTRATSSGEGLEKCGTGHGVPSQFOQWGSNDIAYGVAFSISFVUVERSK 178
 QY 193 -DLRFLMHNNEAHTITSEMVOKRKHMSCTVTCMRLKTAANGVLRKT 250
 Db 179 ASSHLMNHNNBAGKAIIHLTMVECKHGVSCEVKTCWAVYKPKVGHALKKE 238
 QY 251 DGASVNLWKNKSRSRASRLRKEPEPNKPKPSFHULMVEKSTAEISGKTAGT 310
 Db 239 DATEVERFVSSA-----LVPNAVQKPHDEOLVLEPSDFCQDMRSVGLT 291
 QY 311 AGRACNSHAIIDGCELLNGRRGHRTRQRTENCFHWCHVIS'NTHTWLHC 369
 Db 292 KGRTCNKSKAIDGCELLCGGRGHTAALVAFERSCKHWOCFVKPLQURVELHC 350
 RESULT 8
 US-10-175-737-80
 ; Sequence 80, Application US/10175737
 ; Publication No. US2003013153A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Chen, Jian

QY 311 AGRAGNSSPALDGECELLCGRHTKTRQTYTERNCFHWCHNSCRNTHRLHEC 369
Db 292 RGRTCNKTSKAIDGCCELLCGRGFHTAQVELAERCSCFHCCFVRCROCORVELHC 350

RESULT 12
US-10-176-482-80
; Sequence 80, Application US/10176482
; Publication No. US20030022296A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Andrej
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanae, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430RC086
; CURRENT APPLICATION NUMBER: US/10176,757
; CURRENT FILING DATE: 2002-06-20
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO: 80
; LENGTH: 351
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-10-176-482-80

Query Match 41 3%; Score 840; UB 3; Length 351;
Best Local Similarity 44.8%; Pred. No. 1.1e-69;
Matches 161; Conservative 55; Mismatches 123; Indels 20; Gaps 4;
Matches 161; Conservative 55; Mismatches 123; Indels 20; Gaps 4;

QY 14 TLLILAKATPAAIANSASSKHWGIVNVAASSINLTISKSLQVLEPSLQLSKRKLIR 73
Db 9 SURLIVFAVSAASN----WLYLAKUSVGSISSEETCE---KLGIGRQWCK 58

QY 74 QNPGLHSYSGJQSQAVERCKWERNERWNPTAPGPHLKFIVNGRCRETAFFATSA 133
Db 59 RNLWMDNRKORAAQIEECOYQERNERNWNSTDLSVPGKVWQGTEAAWVIASSA 118

QY 134 GYTHSVAKSISGSISCTCYDRGKGSPGWHGCSUNIDFGLEHNEFVESEGEKGK- 192
Db 119 GVAFAVTRASSGEGEKGCGTQHGVSPQGQSGCNTAYGAESASFVDPREPSKG 178

QY 193 -DLFPLMLHNNEAGRTTVESEMROECKHMGSCNTVRTWMLFTKAVGIVLFDRF 250
Db 179 ASSRALMHLHNNEAKRALLHMKVCKGVSCEVKTCWRAPFEPQVHALKEF 238

QY 251 DGSARVLYNEGSNRAEPLLLEPEDPAHKPPHDPOLYVYEKSPNITYSGRAGT 310
Db 235 DGAIEVERPVKWSKA-----LPVPAQKPKHDECVLVESETIJDAMESVNLGT 291

QY 311 AGRAGNSSPALDGECELLCGRHTKTRQTYTERNCFHWCHNSCRNTHRLHEC 369
Db 292 RGRTCNKTSKAIDGCCELLCGRGFHTAQVELAERCSCFHCCFVRCROCORVELHC 350

RESULT 14
US-10-176-913-80
; Sequence 80, Application US/10176913
; Publication No. US20030022298A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Andrej
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanae, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430RC056
; CURRENT APPLICATION NUMBER: US/10-176,913
; CURRENT FILING DATE: 2002-06-20
; Prior Application removed - See file wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO: 80
; LENGTH: 351
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-10-176-913-80

Query Match 41 3%; Score 840; UB 3; Length 351;
Best Local Similarity 44.8%; Pred. No. 1.1e-69;
Matches 161; Conservative 55; Mismatches 123; Indels 20; Gaps 4;

QY 14 TLLILAKATPAAIANSASSKHWGIVNVAASSINLTISKSLQVLEPSLQLSKRKLIR 73
Db 9 SURLIVFAVSAASN----WLYLAKUSVGSISSEETCE---KLGIGRQWCK 58

QY 74 QNPGLHSYSGJQSQAVERCKWERNERWNPTAPGPHLKFIVNGRCRETAFFATSA 133
Db 59 RNLWMDNRKORAAQIEECOYQERNERNWNSTDLSVPGKVWQGTEAAWVIASSA 118

QY 134 GYTHSVAKSISGSISCTCYDRGKGSPGWHGCSUNIDFGLEHNEFVESEGEKGK- 192
Db 119 GVAFAVTRASSGEGEKGCGTQHGVSPQGQSGCNTAYGAESASFVDPREPSKG 178

QY 193 -DLFPLMLHNNEAGRTTVESEMROECKHMGSCNTVRTWMLFTKAVGIVLFDRF 250
Db 179 ASSRALMHLHNNEAKRALLHMKVCKGVSCEVKTCWRAPFEPQVHALKEF 238

QY 251 DGSARVLYNEGSNRAEPLLLEPEDPAHKPPHDPOLYVYEKSPNITYSGRAGT 310
Db 235 DGAIEVERPVKWSKA-----LPVPAQKPKHDECVLVESETIJDAMESVNLGT 291

QY 311 AGRAGNSSPALDGECELLCGRHTKTRQTYTERNCFHWCHNSCRNTHRLHEC 369
Db 292 RGRTCNKTSKAIDGCCELLCGRGFHTAQVELAERCSCFHCCFVRCROCORVELHC 350

RESULT 13
US-10-176-757-80
; Sequence 80, Application US/10176757
; Publication No. US20030022297A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Andrej
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanae, Colin K.
; APPLICANT: Wood, William I.

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; LENGTH: 351
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-10-176-911-80
Query Match 41.3%; Score 840; DB 9; Length 351;
Best Local Similarity 44.8%; Pred. No. 1.e-69; Matches 161; Conservative 55; Mismatches 123; Indels 20; Gaps 4;
Matches 161; Conservative 55; Mismatches 123; Indels 20; Gaps 4;
QY 14 TLLALALALPALAANNSGRWGVINNASSNLTDKSLQIVLFLPSLQLLRQRITI 73
Db 9 SRLLIVFAVPSAASN----WLYLKLSVGSISSEETCE----KUQLIQDQVOMCK 58
Db 74 QNFGILHVSGLQAVRECKKOFNRWRNCPAPGHFLSKTRNGCETAFATSA 133
Db 59 RNLEVM(SVRGAQALIECQDFQRFRWRNCLDSLEVFVKVQGTFEARFYA 118
Y 134 GVTHSVARSCSEGTSCTCDYRRGGPDWKGGSNDTDFGRLFGEFVGKGR- 192
Db 119 GVAFAVTRACSGELEKCDCRVHPSQGFGQNSGSENTAYGAFSQFDVRSK 178
QY 193 -DIRFLNLINNEARTVFSMRDCKHMGSTVRCWMLPTIRGDVDR 250
Db 179 ASSRALMLNNEGRRAILTHMRPECKHGSGEVKICWRAPPRQVHALKEK 238
QY 251 DGASRVLVGNRGSNIAKSRELLRLEDPAHKPPSPHULVFEKPNPFTYSGRLTAGT 310
Db 239 DGADEVPRVGSVA----LVPRNAQFKPHIDELVNLIFSPFEDQMSVGLT 291
QY 311 AGRNASSSPALDGEELCCGGRHRRTQVTERCNCFHWCHUSRNTHYRHEC 369
Db 292 RGRTRNKRKAIDGEELCCGGRHTAQVELAERCSTKHFCCFVKRCQJRLVELHT 350
RESULT 15
US-10-180-552-80
; Sequence 80, Application US/10180552
; Publication No US20030022300A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Inc.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P43.081C153
; CURRENT APPLICATION NUMBER: US/10/180,552
; CURRENT FILING DATE: 2007-06-25
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 80
; LENGTH: 351
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-10-180-552-80

Query Match 41.3%; Score 840; DB 9; Length 352;
Best Local Similarity 44.8%; Pred. No. 1.e-69; Matches 161; Conservative 55; Mismatches 123; Indels 20; Gaps 4;
Matches 161; Conservative 55; Mismatches 123; Indels 20; Gaps 4;
QY 14 TLLALALALPALAANNSGRWGVINNASSNLTDKSLQIVLFLPSLQLLRQRITI 73
Db 9 SRLLIVFAVPSAASN----WLYLKLSVGSISSEETCE----KUQLIQDQVOMCK 58
Db 74 QNFGILHVSGLQAVRECKKOFNRWRNCPAPGHFLSKTRNGCETAFATSA 133

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Run on:	April 22, 2003, 16:37:37 : Search time 46 Seconds			
	(without alignments)			
	773,255 Million cell updates/sec			
Title:	US-09-674-292-1			
Perfect score:	2036			
Sequence:	I MGIVAWLPGWGSATILLAAV..... WCHVHSRGNTHTRVLHEG.. 370			
Scoring table:	BIGSTIM52			
Gapop:	10.0 , Gapext: 0.5			
searched:	283224 seqs, 96154422 residues			
Total number of hits satisfying chosen parameters:	283224			
Minimum DB seq length:	0			
Maximum DB seq length:	2000000000			
Post-processing:	Minimum Match 0%			
	Maximum Match 100%			
	Listing first 45 summaries			
Database :	PIR_73;*			
	1: pir1;*			
	2: pir2;*			
	3: pir3;*			
	4: pir4;*			
Pred. No.	is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.			
SUMMARIES				
Result No.	Score	Query Length	DB ID	Description
1	2036	100.0	370	1 TWHITI
2	2021	99.3	370	1 TWMSTI
3	2021	99.3	370	1 TWMTWI
4	1671	82.1	369	2 S13721
5	1595	78.3	370	2 S15013
6	1463	71.9	371	1 TVXLTI
7	1022.5	50.2	468	2 A29550
8	998	49.0	469	1 TVFETI
9	873.5	42.9	552	2 A49146
10	865.5	42.5	303	2 S41156
11	843.5	41.4	352	2 A39332
12	836	41.4	351	2 C36170
13	836	41.1	351	2 JC2451
14	827	40.5	351	2 A48928
15	822.5	40.4	352	2 JC7654
16	787.5	38.7	365	2 JC7654
17	785	38.6	360	2 S00334
18	781	38.4	360	2 B36170
19	780.5	38.3	364	2 F36170
20	769	37.8	379	2 D36170
21	766.5	37.6	365	2 A48914
22	766.5	37.5	372	2 TO9612
23	759	37.3	313	2 TWHITI
24	753	37.0	359	2 A56149
25	749	36.8	372	2 E36170
26	742	36.4	4117	2 B59192
27	741	36.4	4117	2 JC7654
28	728.5	35.8	357	2 B56549
29	728.5	35.6	360	2 S34173

Db 361 THRVLHECL 370

RESULT 2

TMHL transforming protein int-1 - mouse

N; Alternate name: Wnt-1 protein

F; Species: Mus musculus (house mouse)

C; Date: 17-Mar-1987 #sequence-revision 17-Mar-1987 #text-change 18-Jun-1999

C; Accession: A2347; A36470; G0158

R; Fung, Y.K.T.; Shackleford, A.M.; Brown, A.M.; Sanders, G.S.; Varmus, H.E.

Mol. Cell. Biol. 5, 3337-3344, 1985

A; Title: Nucleotide sequence and expression in vitro of cDNA derived from mRNA of int-1, a tumor promoter gene

A; Reference number: A93058; MVID:86310810; PMID:3295519

A; Molecule type: mRNA

A; Cross-references: GB:MI1943; NID:9198423; PIEN:AAA19322_1; PID:9293671

A; Note: the authors translated the codon GTG for residue 242 as Gly and GGC for codon 243; Genin, B.J.; McMahon, J.A.; McMahon, A.P.

Genes Dev. 4, 2315-2332, 1990

Title: Expression of multiple novel Wnt-1/int-1-related genes during fetal and adult mouse brain

A; Accession: A36470; MVID:9122634; PMID:2279700

A; Status: preliminary: nucleic acid sequence not shown; not compared with conceptual translation

A; Molecule type: mRNA

A; Residues: 1-370 <GAV>

C; Genetics:

A; Gene: int-1

A; Introns: 35/2; 126/1; 208/3

C; Superfamily: int-1 transforming protein

C; Keywords: proto-oncogene; transforming protein; transmembrane #status predicted <TM>

Query Match 99.9%; Score 2021; DB 1; Length 370;

Best Local Similarity 98.9%; Pred. No. 3.1e-159;

Matches 366; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Query 1 MQLWALLPSWNTLALAPALANASSGRWGVINAVASSTNLISRSKLSQVLLEPS 60

Db 1 MQLWALLPSWNTLALAPALANASSGRWGVINAVASSTNLISRSKLSQVLLEPS 60

Query 61 IQLLSRKQRRLIRQNFGILHVSGLSAVRECKWKFRRRNCPTAIFHLFSKIVNG 120

Db 61 IQLLSRKQRRLIRQNFGILHVSGLSAVRECKWKFRRRNCPTAIFHLFSKIVNG 120

Query 121 CRETAFIAIT-SAGVHVSARSTSEGSEGSTESTCCTYERKPGPDKWV;PSDNIDFRIF 180

Db 121 CRETAFIAIT-SAGVHVSARSTSEGSEGSTESTCCTYERKPGPDKWV;PSDNIDFRIF 180

Query 181 QREVFESIERSKDRFLRNHNNEAKITVSEMOCECKHMSGS;VFTCMRLLTR 240

Db 181 QREVFESIERSKDRFLRNHNNEAKITVSEMOCECKHMSGS;VFTCMRLLTR 240

Query 241 AVGDVLRRDPSKRLPEPAHKFSPRIIDVFEESPNT 300

Db 241 AVGDVLRRDPSKRLPEPAHKFSPRIIDVFEESPNT 300

Query 301 YSGRJGTTAGACNSSSPAIDCCELCGCGHTRTORYVERNC;FNGCWSPPNC 360

Db 301 YSGRJGTTAGACNSSSPAIDCCELCGCGHTRTORYVERNC;FNGCWSPPNC 360

Query 61 LOLSRKRQPLRFLRONGLIGHSVSGLOSSAVRECKWKFRRRNCPTAIFHLFSKIVNG 120

Db 61 LOLSRKRQPLRFLRONGLIGHSVSGLOSSAVRECKWKFRRRNCPTAIFHLFSKIVNG 120

Query 121 CRETAFIAIT-SAGVHVSARSTSEGSEGSTESTCCTYERKPGPDKWV;PSDNIDFRIF 180

Db 121 CRETAFIAIT-SAGVHVSARSTSEGSEGSTESTCCTYERKPGPDKWV;PSDNIDFRIF 180

RESULT 4

S13721 4

Wnt-1 protein precursor, secreted - axiotl

C; Species: Ambystoma mexicanum (Axolotl)

C; Date: 21-Nov-1993 #sequence-revision 10-Nov-1995 #text-change 16-Jul-1999

C; Accession: S13721; S13722

R; Busse, U.; Guay, J.; Seguin, C.

Nucleic Acids Res. 18, 7431, 1990

A; Title: Nucleotide sequence of a cDNA encoding Wnt-1 of the Mexican axolotl Ambystoma mexicanum

A; Reference number: S13721; MVID:9108334; PMID:259533

A; Status: preliminary: nucleic acid sequence not shown; translation not shown

A; Molecule type: mRNA

A; Residues: 1-369; B052

A; Cross references: EMBL:X55270; NID:96244; PIEN:CAN89C; HUHG2425

R; Busse, U.; Gray, T.; Seguin, C.

Nucleic Acids Res. 19, 981-1001

A; Reference number: S13722; MVID:91204483; PMID:2013933

A; Title: Nucleotide sequence of a cDNA encoding Wnt-1 of the Mexican axotol Ambystoma mexicanum

A; Contents: annotation: reprinted sequence figure

A; Gene: Wnt-1

RESULT 3

TMHL transforming protein int-1 - mouse mammary tumor virus

C; Species: mouse mammary tumor virus. MMTV

C; Date: 31-Dec-1991 #sequence-revision 31-Dec-1991 #text_change 18-Jun-1999

A; Experimental source: neurula stage embryos	Qy 163 -.-.PWHWGCSENIDFGRLGKFVDFSGERKDRFLPHLNHNHEASRTYFSEMQ 216
A; Note: sequence extracted from NCBI backbone (NCBIP:117112)	Db 61 GALASYRVEFWEGCGSNEIGFGFTVSREFVDAEGERKTIREKMLNNEAERWVHLDQ 120
R; Christian, J.L.; Gavin, B.J.; McMahon, A.P.; Moon, R.T.	Db 217 ECKCHIMSSCVRTRWMRFTLAVGIVDLEDFDCAEWVY--MEGSNA----- 266
Dev. Biol. 142: 210-224, 1991	Accession: C49764
A; Reference number: A49764; MUID:9112437; PMID:1991549	A; Status: preliminary
A; Accession: C49764	A; Molecule type: mRNA
A; Residues: 265-295, H' 297-335 <CHR>	A; Cross-references: GB:M5055
C; Superfamily: int-1 transforming protein	Query Match 42.9%; Score 873.5; DB 2; Length 352;
Best Local Similarity 44.6%; Pred. No. 1.5e-64; Mismatches 164; Conservative 62; Indels 21; Gaps 5;	Matches 164; Conservatve 62; Mismatches 121; Indels 21; Gaps 5;
Qy 6 LIPGWSWATLIALAALPAALAANSRGWGVNVNASSNLTDTSKLVLLESLQLS 65	Db 1 MTPEFLRSLMLMILAVFSANASN---WYLAKLSVGSISSEETCEKLGK---I 50
Qy 65 RKQRERLIRNPGLIHSV35GLOSAVRCKWQFRNRWRCPATAPGHLFKEVGRGCRE 124	Db 161 PRKINASISSNSHRSKRERKHYFJLKPFENPEHFKFSTKLVVYVSPSPKPKENFKLGI 240
Db 51 QROVDMCRKRNLEMMOSVRAQLAIEQYQFERNRWNISTLDGNOWFGKILNRGFEA 110	Qy 349 ACTAFAKISSSSPALKCHGAGCTGSHTRTFRVERGNTTHRSJHSVFNCHTRLH 367
Qy 125 AFIFRITAGVHVSARVSSEGESESTCTGURPRPGPDWIGGSDNIDFGFLGEE 184	Db 121 ECKCHIMSCSTIKTWMRFLPFVIGDLKURFDGASWASJHEHNNNAHONPKN 186
Db 111 AFVIAITSGVTHSVIRACSGDLEKRCGCDRIVHGVSPOGFOMSGSDANLYGVAFSSU 170	Qy 267 -----SRARILP----LEPEPAHRPSHULWEEKSFNEYSGRIFT 307
Qy 185 VDSGK--GROLRFMLNNEAGRATVSEMPRECHGSGSCVYRWMPLPTRA 241	Db 181 PRKINASISSNSHRSKRERKHYFJLKPFENPEHFKFSTKLVVYVSPSPKPKENFKLGI 240
Db 171 VDVRERSKGSSSSRAALMNLNEAGRKALLNMRVECKCHGVSSEKVWCKWAMF-FRK 230	Qy 349 ACTAFAKISSSSPALKCHGAGCTGSHTRTFRVERGNTTHRSJHSVFNCHTRLH 367
Qy 242 VGDVDRDREGASRVLYCNNGSNHASPAAELPLPTECAHKPSPHLWIFERKPNFY 341	Db 241 WGHFLRNUSTMVLTUMGSGRJYRTUEVWVFERCNSTIFWJEFVKLWCPKTRH 366
Db 231 VGNVLRKEKGDALEVEQQKAGSTV-----LVRNSQPKPIDEVULVLDSSPDEH 283	Qy 368 EELI 371
Qy 302 SGRITAGTAGACAGNSSPADGEGULCGGHRHTQVTERCNCNPFHWCHYSCRUT 361	Db 301 TCV 303
Db 284 DLKNQVLTGTTGRDNKRNKAIDGELMWCGRHTEEEVETEVES-SKHWCFVKUCH 343	RESULT 11
Qy 362 HTRVHIC 369	A; Residues: 1-352, FJE
Db 344 KVVERHIC 351	A; Cross-references: 53:X5642; MUID:55433; PIUN:2RA4; No. 515; P15:455434
RESULT 10	C; Superfamily: int-1 transforming protein
S41156 wingless protein - red flour beetle (fragment)	Query Match 41.4%; Score 843.5; DB 2; Length 452;
C; Species: Tribolium castaneum (red flour beetle)	Best Local Similarity 45.3%; Pred. No. 4.Be-62; Mismatches 5; Conservative 5; Indels 11; Gaps 4;
C; Date: 07-Sep-1994 #sequence-revision 19-Apr-1995 #text_change 16-Feb-1997	Matches 161; Conservatve 5; Mismatches 5; Indels 11; Gaps 4;
R; Nagy, L.M.; Carroll, S.	Db 7 LIAVLISLKL---GSPYTWLAVESQASS-----STG-----GTPKLFRCNY 59
Nature 367, 450-451, 1994	Qy 16 VHAIAAFLAALANSRHWVTVVASSNLTDTSKLVLLESLQLS 75
A; Title: Conservation of wingless patterning functions in the short-germ embryos of Tribolium castaneum	Db 60 VEIMSVAVGKGIGQDQHDFHFRMNTVTSNLTKSISLVESSLISFKPHFLRQN 75
A; Reference number: S41156; MUID:94150623; PMID:8107804	Qy 115 VTHSVAKSSSEGESESTCTGURPRPGPDWIGGSDNIDFGFLGEE 194
A; Accession: S41156	Db 120 WAFAVTFSAESSAATVSSPGLGSPSEGKGWSELETSMSRPAIENRKA 179
A; Status: not compared with conceptual translation	Qy 76 FGILHVSGLOSAVREKQAFENFRNCPATGP-HLFKRNPN-3-KERAFIAISAG 134
A; Molecule type: mRNA	Db 60 VEIMSVAVGKGIGQDQHDFHFRMNTVTSNLTKSISLVESSLISFKPHFLRQN 75
A; Residues: 1-363 <NAG>	Qy 195 KFLNQHNNHEASITVSEQUECHRSGSCTVWQHTRKAVGFLRQFATGAS 254
C; Genes: wg	Db 180 EKAMHNHHNEAGSCTASHMLKQHOLSGSECTWRSKFLFQHFKYUDAS 239
C; Superfamily: int-1 transforming protein	Qy 255 KLVVYHGSNSRAAELPLK-BEPEAHKPPSHDLYVFKENF-TYSGRUHTAGKA 314
Query Match 42.6%; Score 866.5; DB 2; Length 363;	Db 240 IAVV-----EKKRERKJWVHLKETVWPKFPEWVYKAYSTK-ERMEGKTRT 296
Best Local Similarity 53.5%; Pred. No. 5.1e-64; Mismatches 39; Conservative 39; Indels 41; Gaps 6;	RESULT 12
Matches 162; Conservatve 39; Mismatches 61; Indels 41; Gaps 6;	A35503
Qy 109 GPHLGKTYN3GRETAFIAFAITSGVTHSARVSSEGESESTCD--YIRR---3PGG 162	Wnt3 protein - mouse
Db 1 GKNLFGKIVDKS3ETTAFLYVTAATACSESSIDONCETHYKRPVHSNGG 60	C; Species: Mus musculus (house mouse)
Accession: A45963	C; Date: 09-Nov-1996 #sequence-revision 05-Nov-1996 #text_change 16-Jul-1993

C;Accession: A48828
 R;World, S.L.; Moody, C.J.; Moon, R.T.
 Dev. Biol. 155, 46-57, 1993
 A;Title: Overlapping expression of Xwnt-3A and Xwnt-1 in neural tissue of Xenopus laevis
 A;Reference number: A48828; MUID:93106316; PMID:8416844
 A;Accession: A48828
 A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptua;
 A;Molecule type: mRNA
 A;Residues: 1-352 <WOR>
 A;Note: sequence extracted from NCBI backbone (N:81P:12134)
 C;Superfamily: int-1 transforming protein

Query	Match	Score	822.5;	DB	2;	Length	352;
BEST LOCAL SIMILARITY	43.48	PRED. NO.	2.6e-60;				
MATCHES	154;	CONSERVATIVE	57;	MISMATCHES	133;	INDELS	11;
QY	16	LIAALAPAAUANNSGRWGIYVNVAASSTNLDSKSLULYEPSELQSLRSKORRILRN	75	DB	7	LLLIGLHQVALIPI-WWSLAVGQOYSLGT---QFPCSTIPGLVAKQMRFCNRY	59
QY	76	PGILHSVSGIQSVAECKWPERNRWNPITA-PGPHLGKIVRSCETATIFATSAQ	134	DB	60	MEIMPSVAECKWIGIQEYOHURGRKRNTIVNUNLAFSPVILKATRESAFVHATASQ	119
QY	135	VHHSVARSCCGSIESTCDPYYRRPGPWHWGGSDNDFGRFGFGEFVSGEGKR	194	DB	120	TAVALVIRSCBASATICGODCHTRHKPGEWKQWGSQEDMUGKNSVSEFADARPO	179
QY	195	RFLMLNHNEAERTIVSEMRAVECKCHGMGSATVRCOMPLPTIRAVLUVLRDGDAS	254	DB	180	RSAMRNHNNEAJRTSILDRHRLKCKCHGSGCEVKTOWSUSPFLRVIGTYLKUKYDSAS	239
QY	255	RVLGNRGSNRASRAELRLEEDPRHKPKPSPDVLFERSPNPCFTYSGRLTAGTGRA	314	DB	240	EMVY---EKHRESKOWVETTRPKYTFKKPPIERDLYTTESPNRCPEPNFETGSDRE	296
QY	315	CNSSSFLADGELCCGROHRTRQTCRTERCNGTFCACCHVSCRCNTHVRLHG	369	DB	297	CNTSHDIDGDDLGCGRQNTTERKEKCHCFHQCVCVSYSCORMVRVYDHIC	351

Search completed: April 22, 2003, 16:42:15
Job time : 47 secs

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Title:	GenCore version 5.1.4-p5.4578
Copyright (c) 1993 - 2003 Compugen Ltd.	
OM protein - protein search, using sw model	
Run on:	April 22, 2003, 16:28:42 ; Search time 25 Seconds
Post-processing:	(without alignments)
Scoring table:	BLASTM2
Searched:	112892 seqs, 41476328 residues
Total number of hits satisfying chosen parameters:	112892
Minimum DB seq length:	0
Maximum DB seq length:	200000000
Post-processing:	Minimum Match 0%
Database :	SwissProt;40,*
pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	8
Result No.	Query Match Length DB ID Description
1	100.0 370 1 WNT1_HUMAN P04528 homo sapien
2	99.3 370 1 WNT1_MOUSE P04426 mus musculus
3	82.1 369 1 WNT1_AMBRE P21551 ambystoma m
4	78.3 370 1 WNT1_BRARE P24257 brachydanio
5	71.9 371 1 WNT1_XENIA P10108 xenopus lae
6	52.2 392 1 WNT1_BOMBO P49340 bombyx mori
7	50.2 468 1 WNT1_DROME P09515 drosophil
8	41.4 352 1 WNT3A_MOUSE P27467 mus musculus
9	843.5 355 1 WNT3_MOUSE P17553 mus musculus
10	843.5 351 1 WNT4_XENIA P49338 xenopus lae
11	47.3 355 1 WNT3_HUMAN P56703 homo sapien
12	41.3 351 1 WNT4_HUMAN P56705 homo sapien
13	836 41.1 351 1 WNT4_MOUSE P22724 mus musculus
14	836 41.1 351 1 WNT4_RAT P09x95 rattus norv
15	832 40.9 351 1 WNT4_CHICK P49337 gallus galli
16	82.5 40.6 352 1 WNT4_HUMAN P56704 homo sapien
17	82.5 40.4 352 1 WNT3A_XENIA P31285 xenopus lae
18	82.5 40.3 352 1 WNT4_BRAKE P47793 brachydanio
19	815.5 40.1 223 1 WNT1_STREPO P28094 streptococc
20	79.9 391 1 WNT2B_HUMAN Q93097 homo sapien
21	87.5 387 1 WNT5_HUMAN Q9Y6f9 homo sapien
22	78.5 360 1 WNT2_HUMAN P09544 homo sapien
23	78.4 38.5 389 1 WNT2B_MOUSE P070283 mus musculus
24	78.1 38.4 360 1 WNT2_MOUSE P21552 mus musculus
25	78.0.5 38.3 364 1 WNT6_MOUSE P22727 mus musculus
26	77.2 37.9 351 1 WNT2B_XENIA P87387 xenopus lae
27	77.2 37.9 379 1 WNT5A_RAT Q9QX97 rattus norv
28	76.9 37.8 379 1 WNT5A_MOUSE P22726 mus musculus
29	76.5 37.6 365 1 WNT5A_HUMAN P41221 homo sapien
30	76.2 37.5 371 1 WNT5A_XENIA P41222 orizias lat
31	76.0 37.3 350 1 WNT2_BRACE P092043 brachydanio
32	75.8 37.2 359 1 WNT5A_PLWA P03297 pseudepis
33	75.4 37.1 380 1 WNT5A_XENIA P31286 xenopus lae
Result No.	ALIGNMENTS
1	WNT1_HUMAN STANDARD: FRT; 370 AA.
2	WNT1_HUMAN P04528: FRT; 370 AA.
3	WNT1_HUMAN P04426: FRT; 370 AA.
4	WNT1_BRARE P21551: FRT; 370 AA.
5	WNT1_XENIA P10108: FRT; 370 AA.
6	WNT1_BOMBO P49340: FRT; 370 AA.
7	WNT1_DROME P09515: FRT; 370 AA.
8	WNT3A_MOUSE P27467: FRT; 370 AA.
9	WNT3_MOUSE P17553: FRT; 370 AA.
10	WNT4_XENIA P49338: FRT; 370 AA.
11	WNT3_HUMAN P56703: FRT; 370 AA.
12	WNT4_HUMAN P56705: FRT; 370 AA.
13	WNT4_MOUSE P22724: FRT; 370 AA.
14	WNT4_RAT P09x95: FRT; 370 AA.
15	WNT4_CHICK P49337: FRT; 370 AA.
16	WNT4_HUMAN P56704: FRT; 370 AA.
17	WNT3A_XENIA P31285: FRT; 370 AA.
18	WNT4_BRAKE P47793: FRT; 370 AA.
19	WNT1_STREPO P28094: FRT; 370 AA.
20	WNT2B_HUMAN Q93097: FRT; 370 AA.
21	WNT5_HUMAN Q9Y6f9: FRT; 370 AA.
22	WNT2_HUMAN P09544: FRT; 370 AA.
23	WNT2B_MOUSE P070283: FRT; 370 AA.
24	WNT2_MOUSE P21552: FRT; 370 AA.
25	WNT6_MOUSE P22727: FRT; 370 AA.
26	WNT2B_XENIA P87387: FRT; 370 AA.
27	WNT5A_RAT Q9QX97: FRT; 370 AA.
28	WNT5A_MOUSE P22726: FRT; 370 AA.
29	WNT5A_HUMAN P41221: FRT; 370 AA.
30	WNT5A_XENIA P41222: FRT; 370 AA.
31	WNT2_BRACE P092043: FRT; 370 AA.
32	WNT5A_PLWA P03297: FRT; 370 AA.
33	WNT5A_XENIA P31286: FRT; 370 AA.
Best Local Similarity	Score: 2366; DB: 13; Search: 370;

AC P27467;
 DT 01-AUG-1992 (Rel. 2.3, Created)
 DT 01-AUG-1992 (Rel. 2.3, Last sequence update)
 DT 15-JUN-2002 (Rel. 4.1, Last annotation update)
 DE WNT-3A protein precursor.
 GN WNT3A OR WNT-3A.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciuromorpha; Muridae; Murinae; Mus;
 OX NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RX MEDLINE:91150971; PubMed=2001840;
 RA Roelink H.; Nusse R.;
 RT "Expression of two members of the Wnt family during mouse development -- two restricted temporal and spatial patterns in the developing neural tube.";
 RL Dev. 5: 381-385 (1971)
 CC FUNCTION: LIGAND FOR MEMBERS OF THE FRIZZLED FAMILY OF SEVEN TRANSMEMBRANE RECEPTORS. WNT-3 AND WNT-3A PLAY DISTINCT ROLES IN CELL-CELL SIGNALING DURING MORPHOGENESIS OF THE DEVELOPING NEURAL TUBE.
 CC -!- SUBCELLULAR LOCATION: Possibly secreted and associates with the extracellular matrix.
 CC -!- TISSUE SPECIFICITY: DORSAL PORTION OF THE NEURAL TUBE (DVELOPING ROOF PLATE), AND MESENCHYME TISSUE SURROUNDING THE MBILIAZ VEINS.
 CC -!- SIMILARITY: BELONGS TO THE WNT FAMILY.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation at the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
 CC
 CC PRINTER: PRO010; WNT-1; DR PRINTS; PRO1349; WNTPROTEIN.
 DR SMART: SM00597; WNT1; 1.
 DR PROSITE: PS0245; WNT1; 1.
 AN developmental protein; Glycoprotein; Signal; Extracellular matrix; SIGNAL 1
 FT CHAIN 24 POTENTIAL.
 FT CARBOHYD 25 352 WNT-3A PROTEIN.
 FT 87 N-LINKED (GLCNAC . . .) (POTENTIAL).
 FT 298 N LINKED (GLCNAC . . .) (POTENTIAL).
 SQ SEQUENCE 352 AA: >9257 MW: 74DFC5B38AEFFF63 CRC64;
 Query Match Best Local Similarity 41.4%; Score 843.5; DB 1; Length 352; Matches 161; Conservative 53; Mismatches 130; Indels 11; Gaps 4;
 Qy 16 LLAAALPAALANNSGRMGWIVNVAASSTNLIDSKSLQVLEPLQLSLQRKRLRQN 75
 Db 7 ILLVCSKLAL--GYPYIPLSLAVGPPOSSL----STOPILCASIPGVLPDKATRESAFVHATASAG 59
 Qy 76 PGIIHSUSSGGLOSSAVRECKWQPNRNRNCITARGP-HFEGKVNGRCFATTAIS 134
 Db 60 VEIMPSVVEGYKAGIQECOHQFRGRNCTVVSNLALFGPVLDKATRESAFVHATASAG 119
 Qy 135 VTHVARSCSESDISCTDVRRGCGPDWHGGSNIDEGFLGREFVDUSGEKURDL 194
 Db 120 WAFAVTRACEDSAACGCCGSSRRAQSGEPMGKWWGCGCDEENGMSRFADARENPDAD 179
 Qy 195 RFLMLHNEAGRTVFSERQBCRGHMSCTVTRCMRLPTAVSVLRLRFQGAS 254
 Db 180 RSAMHRHNEAGROIAASHMHLCKHGSGSCVKTWSOPDERTIGDPLKDQYUSAS 239
 RESULT 9
 RN WNT3 MOUSE
 ID WNT3 MOUSE
 STANDART PRT: 455 AA.
 AC P11753;
 DT 01-AUG-1990 (Rel. 1.5, created);
 DT 01-AUG-1990 (Rel. 1.5, Last sequence update);
 DT 15-JUN-2002 (Rel. 4.1, Last annotation update);
 DE WNT-3 protein/secreted protein precursor.
 RN WNT-3A OR WNT-4 OR INT-4.
 CC Mus musculus (mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciuromorpha; Muridae; Murinae;
 OX NCBI_Taxid=10090;
 RN WNT-3A
 PR SEQUENCE FROM N.A.
 RC STRAIN=Balb/c; TISSUE=embryo;
 RX MEDLINE:91150971; PubMed=2001840;
 RA Roelink H.; Wagner E.; Llives J.; Silva S.; Nusse R.;
 RT "Wnt-3, a gene activated by proviral insertion in mouse mammary tumor virus, is homologous to int-1/Wnt-1 and is normally expressed in mouse embryo and adult brain.";
 RL Proc. Natl. Acad. Sci. U.S.A. 87:4515-4523 (1990)
 CC -!- FUNCTION: LIGAND FOR MEMBERS OF THE FRIZZLED FAMILY OF SEVEN TRANSMEMBRANE RECEPTORS. WNT-3 AND WNT-3A PLAY DISTINCT ROLES IN CELL-CELL SIGNALING DURING MORPHOGENESIS OF THE DEVELOPING NEURAL TUBE.
 CC -!- SUBCELLULAR LOCATION: Possibly secreted and associates with the extracellular matrix.
 CC -!- TISSUE SPECIFICITY: DORSAL PORTION OF THE NEURAL TUBE, DORSAL ECTODERM, THE BRANCHIAL ARCS, AND THE LIME KLS.
 CC -!- DISEASE: SOME MOUSE MAMMARY TUMORS INDUCED BY MOUSE MAMMARY TUMOR VIRUS (MMTV) CONTAIN A PROVIRUS INTEGRATE IN A HOST CELL REGION WHICH HAS BEEN NAMED WNT-3.
 CC -!- SIMILARITY: BELONGS TO THE WNT FAMILY.
 CC
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 CC
 DR EMBL: M37502; AAC38109; 1.
 DR PIR: A35542; A35503; 1.
 DR MGI: MGI:9895; Wnt3.
 DR InterPro: IP0000970; Wnt-growthfactor.
 DR PRINTS; PRO1349; WNTPROTEIN.
 DR SMART: SM00597; WNT1; 1.
 DR PROSITE: PS0245; WNT1; 1.
 KW Developmental Protein; Glycoprotein; Signal; Protoponcogene;
 KW Extracellular matrix; Potential.
 FT CHAIN 21 WNT-3 PROTO-ONCOGENE PROTEIN.
 FT CARBOHYD 22 355 N-LINKED (GLCNAC . . .) (POTENTIAL).
 FT 90 301 355 MW: 73176584901; GAPS: 4;
 SQ SEQUENCE 355 AA: >9259 MW: 73176584901; GAPS: 4;
 Query Match Best Local Similarity 41.4%; Score 843.5; DB 2; Length 355; Matches 155; Conservative 53; Mismatches 123; Indels 9; Gaps 3;

DR EMBL:AY009496; ARB3658 1; -->
 DR EMBL:AF316943; ARB51699 1; -->
 DR EMBL:AL031281; CAB5201 1; -->
 DR EMBL:AF335591; ARK25765 1; -->
 DR EMBL:AK03657; ARS5042 1; -->
 DR GenBank:HGNC:12283; WNT4
 DR InterPro:IPR000970; Wnt_gtfactor.
 DR PTam:PF00110; wnt_1.
 DR PRINTS:PRO134; WNPOTEN.
 DR SMART:SM00097; WNT1 1.
 DR FROST:PF00245; WNT1 1.
 DR Developmental protein; Glycoprotein; Signal.
 FT SIGNAL 1
 FT CHAIN 23 351
 FT CARBOHYD 88 88
 FT CARBOHYD 297 297
 FT CONFLICT 106 106 T -> I (IN REF. 1).
 FT CONFLICT 111 111 F -> L (IN REF. 1).
 SF SEQUENCE 351 AA; 35051 MW: 465D08755C92DAB CRC64:
 Query Match 41.3%; Score 840; UB 1; Length 351;
 Best Local Similarity 44.8%; Pred. No. 4 9e-6; Gaps 4;
 Matches 161; Conservative 55; Mismatches 123; Idents 20; Gaps 4;
 OY 14 TLLALAAKPLAANSRGWGINVASSNLITLSKQIVLVEPSQLRSKRFLR 73
 Db 9 SRLRYFAVESSAARN----WLYLAKLSSVSISETICE---KLKGIIQVQMK 58
 QY 74 QPGILHSVSGLOSSAREKFGNFRNRCNTAPFPHSKINNGREFAFIATSA 133
 Db 59 RNLLEMDSVRGAQALAECCOYQFRNRWNCSTLDSPVFGKVYTOGTFREAFVYAISSA 118
 QY 134 GYTHSWARSSSEGSIESCTCYRRGGPDWHRGG3UNDEFRLGREFVDSGEKGR- 192
 Db 119 GVAFAVTRACSSSELEKGCRTVQGVSQGCSJSUNIAYVAWSQEDVRSKG 178
 QY 193 -DLRFELNHNNNEAGRITVSEMPQCCHNSGSTVTCRMLPFLRAWDYLDRP 250
 Db 179 ASSRALMHNNEAGKALTHMRVECKHGVSGSTEWTKPAPFRRQGHAIKEF 238
 QY 251 DRSKFLYGRGSGRASHAELRLPEDAHFPHSPHDLYFEESPNTGYSRGTATI 310
 Db 239 DATEVEPRRVGSSRA----LVPRNAQKFHTEDVLYLESPDFEQDMRSGVLT 291
 QY 311 AGRACSSSSALGCCELCCGGRGHRTRTWRVFCNOTEWCIVSNSRNTHTRIHEC 369
 Db 292 RGRICKTSKTAIDGCCLCGCGFHTAQVELAERCSCFKWCVKQFCORLVHLTC 350
 'SULT 13
 14_MOUSE STANDARD: PRT; 351 AA.
 +* WNT4_MOUSE STANDARD: PRT; 351 AA.
 AC P22724;
 DT 01-AUG-1991 (Rel. 19, Created)
 DT 01-AUG-1991 (Rel. 19, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE WNT-4 Protein precursor.
 GN WNT-4 Protein.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBL-TAXID=10040;
 RN [1]
 RP SEQUENCE FROM N_A.
 RX MEDLINE:91122634; PubMed:2279700;
 RA Gavin, B. J.; McMahon, J. A.; McMahon, A. P.;
 RT *Expression of multiple novel Wnt-1/int-1-related genes during fetal
 RT and adult mouse development.,
 RT Genes Dev. 4:2419-2332(1990).
 .-- FUNCTION: LIGAND FOR MEMBERS OF THE FRIZZLED FAMILY OF SEVEN
 .-- TRANSMEMBRANE RECEPTORS. MAY BE AN INTRACELLULAR SIGNALING
 MOLECULE INVOLVED IN SEGMENTATION OF THE FOREBRAIN. IS LIKELY TO
 CC SIGNAL OVER ONLY FER CELL. DIAMETERS (BY SIMILARITY) SEEKS TO BE
 CC INVOLVED IN KIDNEY DEVELOPMENT.
 CC SUBCELLULAR LOCATION: Possibly secreted and associates with the
 CC extracellular matrix.
 CC TISSUE SPECIFICITY: IN ADULTS IN LUNG AND BRAIN.
 CC SIMILARITY: BELONGS TO THE WNT FAMILY.
 CC
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstat
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 CC use by non-profit institutions as long as its content is in no
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 CC or send an email to license@ebi.ac.uk.
 CC
 DR EMBL: M89717; AAA40564 1; -->
 DR PIR: C64470; C36470
 DR PTam: IPRO00970; wnt_1.
 DR PRINTS: PRO134; WNPOTEN.
 DR SMART: SM00097; WNT1 1.
 DR Developmental protein; Glycoprotein; Signal.
 FT SIGNAL 1
 FT CHAIN 23 351
 FT CARBOHYD 88 88
 FT CARBOHYD 297 297 N-LINKED (GLCNAC -> -) (POTENTIAL).
 SF SEQUENCE 351 AA; 35049 MW: 7675C739E9B9D9 CRC64:
 Query Match 41.1%; Score 836; DB 1; Length 351;
 Best Local Similarity 44.6%; Pred. No. 1 1e-65; Gaps 1;
 Matches 160; Conservative 55; Mismatches 124; Idents 20; Gaps 1;
 OY 14 TLLALAAKPLAANSRGWGINVASSNLITLSKQIVLVEPSQLRSKRFLR 73
 Db 9 SRLRYFAVESSAARN----WLYLAKLSSVSISETICE---KLKGIIQVQMK 58
 QY 74 QPGILHSVSGLOSSAREKFGNFRNRCNTAPFPHSKINNGREFAFIATSA 133
 Db 119 GVAFAVTRACSSSELEKGCRTVQGVSQGCSJSUNIAYVAWSQEDVRSKG 178
 QY 193 -DLRFELNHNNNEAGRITVSEMPQCCHNSGSTVTCRMLPFLRAWDYLDRP 250
 Db 179 ASSRALMHNNEAGKALTHMRVECKHGVSGSTEWTKPAPFRRQGHAIKEF 238
 QY 251 DRSKFLYGRGSGRASHAELRLPEDAHFPHSPHDLYFEESPNTGYSRGTATI 310
 Db 239 DATEVEPRRVGSSRA----LVPRNAQKFHTEDVLYLESPDFEQDMRSGVLT 291
 QY 311 AGRACSSSSALGCCELCCGGRGHRTRTWRVFCNOTEWCIVSNSRNTHTRIHEC 369
 Db 292 RGRICKTSKTAIDGCCLCGCGFHTAQVELAERCSCFKWCVKQFCORLVHLTC 350
 DR EMBL:AY009496; ARB3658 1; -->
 DR EMBL:AF316943; ARB51699 1; -->
 DR EMBL:AL031281; CAB5201 1; -->
 DR EMBL:AF335591; ARK25765 1; -->
 DR EMBL:AK03657; ARS5042 1; -->
 DR GenBank:HGNC:12283; WNT4
 DR InterPro:IPR000970; Wnt_gtfactor.
 DR PTam:PF00110; wnt_1.
 DR PRINTS:PRO134; WNPOTEN.
 DR SMART:SM00097; WNT1 1.
 DR Developmental protein; Glycoprotein; Signal.
 FT SIGNAL 1
 FT CHAIN 23 351
 FT CARBOHYD 88 88
 FT CARBOHYD 297 297 N-LINKED (GLCNAC -> -) (POTENTIAL).
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 OY 14 TLLALAAKPLAANSRGWGINVASSNLITLSKQIVLVEPSQLRSKRFLR 73
 Db 9 SRLRYFAVESSAARN----WLYLAKLSSVSISETICE---KLKGIIQVQMK 58
 QY 74 QPGILHSVSGLOSSAREKFGNFRNRCNTAPFPHSKINNGREFAFIATSA 133
 Db 119 GVAFAVTRACSSSELEKGCRTVQGVSQGCSJSUNIAYVAWSQEDVRSKG 178
 QY 193 -DLRFELNHNNNEAGRITVSEMPQCCHNSGSTVTCRMLPFLRAWDYLDRP 250
 Db 179 ASSRALMHNNEAGKALTHMRVECKHGVSGSTEWTKPAPFRRQGHAIKEF 238
 QY 251 DRSKFLYGRGSGRASHAELRLPEDAHFPHSPHDLYFEESPNTGYSRGTATI 310
 Db 239 DATEVEPRRVGSSRA----LVPRNAQKFHTEDVLYLESPDFEQDMRSGVLT 291
 QY 311 AGRACSSSSALGCCELCCGGRGHRTRTWRVFCNOTEWCIVSNSRNTHTRIHEC 369
 Db 292 RGRICKTSKTAIDGCCLCGCGFHTAQVELAERCSCFKWCVKQFCORLVHLTC 350
 DR EMBL:AY009496; ARB3658 1; -->
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 DR EMBL:AL031281; CAB5201 1; -->
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 DR GenBank:HGNC:12283; WNT4
 DR InterPro:IPR000970; Wnt_gtfactor.
 DR PTam:PF00110; wnt_1.
 DR PRINTS:PRO134; WNPOTEN.
 DR SMART:SM00097; WNT1 1.
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 FT CHAIN 23 351
 FT CARBOHYD 88 88
 FT CARBOHYD 297 297 N-LINKED (GLCNAC -> -) (POTENTIAL).
 SF SEQUENCE 351 AA; 35049 MW: 7675C739E9B9D9 CRC64:
 Query Match 41.1%; Score 836; DB 1; Length 351;
 Best Local Similarity 44.6%; Pred. No. 1 1e-65; DB 1; Length 351;
 Matches 160; Conservative 55; Mismatches 124; Idents 20; Gaps 1;
 OY 14 TLLALAAKPLAANSRGWGINVASSNLITLSKQIVLVEPSQLRSKRFLR 73
 Db 9 SRLRYFAVESSAARN----WLYLAKLSSVSISETICE---KLKGIIQVQMK 58
 QY 74 QPGILHSVSGLOSSAREKFGNFRNRCNTAPFPHSKINNGREFAFIATSA 133
 Db 119 GVAFAVTRACSSSELEKGCRTVQGVSQGCSJSUNIAYVAWSQEDVRSKG 178
 QY 193 -DLRFELNHNNNEAGRITVSEMPQCCHNSGSTVTCRMLPFLRAWDYLDRP 250
 Db 179 ASSRALMHNNEAGKALTHMRVECKHGVSGSTEWTKPAPFRRQGHAIKEF 238
 QY 251 DRSKFLYGRGSGRASHAELRLPEDAHFPHSPHDLYFEESPNTGYSRGTATI 310
 Db 239 DATEVEPRRVGSSRA----LVPRNAQKFHTEDVLYLESPDFEQDMRSGVLT 291
 QY 311 AGRACSSSSALGCCELCCGGRGHRTRTWRVFCNOTEWCIVSNSRNTHTRIHEC 369
 Db 292 RGRICKTSKTAIDGCCLCGCGFHTAQVELAERCSCFKWCVKQFCORLVHLTC 350
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 DR EMBL:AF316943; ARB51699 1; -->
 DR EMBL:AL031281; CAB5201 1; -->
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 DR EMBL:AK03657; ARS5042 1; -->
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 DR PRINTS:PRO134; WNPOTEN.
 DR SMART:SM00097; WNT1 1.
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 FT CHAIN 23 351
 FT CARBOHYD 88 88
 FT CARBOHYD 297 297 N-LINKED (GLCNAC -> -) (POTENTIAL).
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 OY 14 TLLALAAKPLAANSRGWGINVASSNLITLSKQIVLVEPSQLRSKRFLR 73
 Db 9 SRLRYFAVESSAARN----WLYLAKLSSVSISETICE---KLKGIIQVQMK 58
 QY 74 QPGILHSVSGLOSSAREKFGNFRNRCNTAPFPHSKINNGREFAFIATSA 133
 Db 119 GVAFAVTRACSSSELEKGCRTVQGVSQGCSJSUNIAYVAWSQEDVRSKG 178
 QY 193 -DLRFELNHNNNEAGRITVSEMPQCCHNSGSTVTCRMLPFLRAWDYLDRP 250
 Db 179 ASSRALMHNNEAGKALTHMRVECKHGVSGSTEWTKPAPFRRQGHAIKEF 238
 QY 251 DRSKFLYGRGSGRASHAELRLPEDAHFPHSPHDLYFEESPNTGYSRGTATI 310
 Db 239 DATEVEPRRVGSSRA----LVPRNAQKFHTEDVLYLESPDFEQDMRSGVLT 291
 QY 311 AGRACSSSSALGCCELCCGGRGHRTRTWRVFCNOTEWCIVSNSRNTHTRIHEC 369
 Db 292 RGRICKTSKTAIDGCCLCGCGFHTAQVELAERCSCFKWCVKQFCORLVHLTC 350
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 DR EMBL:AF316943; ARB51699 1; -->
 DR EMBL:AL031281; CAB5201 1; -->
 DR EMBL:AF335591; ARK25765 1; -->
 DR EMBL:AK03657; ARS5042 1; -->
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 DR PTam:PF00110; wnt_1.
 DR PRINTS:PRO134; WNPOTEN.
 DR SMART:SM00097; WNT1 1.
 DR Developmental protein; Glycoprotein; Signal.
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 FT CHAIN 23 351
 FT CARBOHYD 88 88
 FT CARBOHYD 297 297 N-LINKED (GLCNAC -> -) (POTENTIAL).
 SF SEQUENCE 351 AA; 35049 MW: 7675C739E9B9D9 CRC64:
 Query Match 41.1%; Score 836; DB 1; Length 351;
 Best Local Similarity 44.6%; Pred. No. 1 1e-65; DB 1; Length 351;
 Matches 160; Conservative 55; Mismatches 124; Idents 20; Gaps 1;
 OY 14 TLLALAAKPLAANSRGWGINVASSNLITLSKQIVLVEPSQLRSKRFLR 73
 Db 9 SRLRYFAVESSAARN----WLYLAKLSSVSISETICE---KLKGIIQVQMK 58
 QY 74 QPGILHSVSGLOSSAREKFGNFRNRCNTAPFPHSKINNGREFAFIATSA 133
 Db 119 GVAFAVTRACSSSELEKGCRTVQGVSQGCSJSUNIAYVAWSQEDVRSKG 178
 QY 193 -DLRFELNHNNNEAGRITVSEMPQCCHNSGSTVTCRMLPFLRAWDYLDRP 250
 Db 179 ASSRALMHNNEAGKALTHMRVECKHGVSGSTEWTKPAPFRRQGHAIKEF 238
 QY 251 DRSKFLYGRGSGRASHAELRLPEDAHFPHSPHDLYFEESPNTGYSRGTATI 310
 Db 239 DATEVEPRRVGSSRA----LVPRNAQKFHTEDVLYLESPDFEQDMRSGVLT 291
 QY 311 AGRACSSSSALGCCELCCGGRGHRTRTWRVFCNOTEWCIVSNSRNTHTRIHEC 369
 Db 292 RGRICKTSKTAIDGCCLCGCGFHTAQVELAERCSCFKWCVKQFCORLVHLTC 350
 DR EMBL:AY009496; ARB3658 1; -->
 DR EMBL:AF316943; ARB51699 1; -->
 DR EMBL:AL031281; CAB5201 1; -->
 DR EMBL:AF335591; ARK25765 1; -->
 DR EMBL:AK03657; ARS5042 1; -->
 DR GenBank:HGNC:12283; WNT4
 DR InterPro:IPR000970; Wnt_gtfactor.
 DR PTam:PF00110; wnt_1.
 DR PRINTS:PRO134; WNPOTEN.
 DR SMART:SM00097; WNT1 1.
 DR Developmental protein; Glycoprotein; Signal.
 FT SIGNAL 1
 FT CHAIN 23 351
 FT CARBOHYD 88 88
 FT CARBOHYD 297 297 N-LINKED (GLCNAC -> -) (POTENTIAL).
 SF SEQUENCE 351 AA; 35049 MW: 7675C739E9B9D9 CRC64:
 Query Match 41.1%; Score 836; DB 1; Length 351;
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 Matches 160; Conservative 55; Mismatches 124; Idents 20; Gaps 1;
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 Db 9 SRLRYFAVESSAARN----WLYLAKLSSVSISETICE---KLKGIIQVQMK 58
 QY 74 QPGILHSVSGLOSSAREKFGNFRNRCNTAPFPHSKINNGREFAFIATSA 133
 Db 119 GVAFAVTRACSSSELEKGCRTVQGVSQGCSJSUNIAYVAWSQEDVRSKG 178
 QY 193 -DLRFELNHNNNEAGRITVSEMPQCCHNSGSTVTCRMLPFLRAWDYLDRP 250
 Db 179 ASSRALMHNNEAGKALTHMRVECKHGVSGSTEWTKPAPFRRQGHAIKEF 238
 QY 251 DRSKFLYGRGSGRASHAELRLPEDAHFPHSPHDLYFEESPNTGYSRGTATI 310
 Db 239 DATEVEPRRVGSSRA----LVPRNAQKFHTEDVLYLESPDFEQDMRSGVLT 291
 QY 311 AGRACSSSSALGCCELCCGGRGHRTRTWRVFCNOTEWCIVSNSRNTHTRIHEC 369
 Db 292 RGRICKTSKTAIDGCCLCGCGFHTAQVELAERCSCFKWCVKQFCORLVHLTC 350
 DR EMBL:AY009496; ARB3658 1; -->
 DR EMBL:AF316943; ARB51699 1; -->
 DR EMBL:AL031281; CAB5201 1; -->
 DR EMBL:AF335591; ARK25765 1; -->
 DR EMBL:AK03657; ARS5042 1; -->
 DR GenBank:HGNC:12283; WNT4
 DR InterPro:IPR000970; Wnt_gtfactor.
 DR PTam:PF00110; wnt_1.
 DR PRINTS:PRO134; WNPOTEN.
 DR SMART:SM00097; WNT1 1.
 DR Developmental protein; Glycoprotein; Signal.
 FT SIGNAL 1
 FT CHAIN 23 351
 FT CARBOHYD 88 88
 FT CARBOHYD 297 297 N-LINKED (GLCNAC -> -) (POTENTIAL).
 SF SEQUENCE 351 AA; 35049 MW: 7675C739E9B9D9 CRC64:
 Query Match 41.1%; Score 836; DB 1; Length 351;
 Best Local Similarity 44.6%; Pred. No. 1 1e-65; DB 1; Length 351;
 Matches 160; Conservative 55; Mismatches 124; Idents 20; Gaps 1;
 OY 14 TLLALAAKPLAANSRGWGINVASSNLITLSKQIVLVEPSQLRSKRFLR 73
 Db 9 SRLRYFAVESSAARN----WLYLAKLSSVSISETICE---KLKGIIQVQMK 58
 QY 74 QPGILHSVSGLOSSAREKFGNFRNRCNTAPFPHSKINNGREFAFIATSA 133
 Db 119 GVAFAVTRACSSSELEKGCRTVQGVSQGCSJSUNIAYVAWSQEDVRSKG 178
 QY 193 -DLRFELNHNNNEAGRITVSEMPQCCHNSGSTVTCRMLPFLRAWDYLDRP 250
 Db 179 ASSRALMHNNEAGKALTHMRVECKHGVSGSTEWTKPAPFRRQGHAIKEF 238
 QY 251 DRSKFLYGRGSGRASHAELRLPEDAHFPHSPHDLYFEESPNTGYSRGTATI 310
 Db 239 DATEVEPRRVGSSRA----LVPRNAQKFHTEDVLYLESPDFEQDMRSGVLT 291
 QY 311 AGRACSSSSALGCCELCCGGRGHRTRTWRVFCNOTEWCIVSNSRNTHTRIHEC 369
 Db 292 RGRICKTSKTAIDGCCLCGCGFHTAQVELAERCSCFKWCVKQFCORLVHLTC 350
 DR EMBL:AY009496; ARB3658 1; -->
 DR EMBL:AF316943; ARB51699 1; -->
 DR EMBL:AL031281; CAB5201 1; -->
 DR EMBL:AF335591; ARK25765 1; -->
 DR EMBL:AK03657; ARS5042 1; -->
 DR GenBank:HGNC:12283; WNT4
 DR InterPro:IPR000970; Wnt_gtfactor.
 DR PTam:PF00110; wnt_1.
 DR PRINTS:PRO134; WNPOTEN.
 DR SMART:SM00097; WNT1 1.
 DR Developmental protein; Glycoprotein; Signal.
 FT SIGNAL 1
 FT CHAIN 23 351
 FT CARBOHYD 88 88
 FT CARBOHYD 297 297 N-LINKED (GLCNAC -> -) (POTENTIAL).
 SF SEQUENCE 351 AA; 35049 MW: 7675C739E9B9D9 CRC64:
 Query Match 41.1%; Score 836; DB 1; Length 351;
 Best Local Similarity 44.6%; Pred. No. 1 1e-65; DB 1; Length 351;
 Matches 160; Conservative 55; Mismatches 124; Idents 20; Gaps 1;
 OY 14 TLLALAAKPLAANSRGWGINVASSNLITLSKQIVLVEPSQLRSKRFLR 73
 Db 9 SRLRYFAVESSAARN----WLYLAKLSSVSISETICE---KLKGIIQVQMK 58
 QY 74 QPGILHSVSGLOSSAREKFGNFRNRCNTAPFPHSKINNGREFAFIATSA 133
 Db 119 GVAFAVTRACSSSELEKGCRTVQGVSQGCSJSUNIAYVAWSQEDVRSKG 178
 QY 193 -DLRFELNHNNNEAGRITVSEMPQCCHNSGSTVTCRMLPFLRAWDYLDRP 250
 Db 179 ASSRALMHNNEAGKALTHMRVECKHGVSGSTEWTKPAPFRRQGHAIKEF 238
 QY 251 DRSKFLYGRGSGRASHAELRLPEDAHFPHSPHDLYFEESPNTGYSRGTATI 310
 Db 239 DATEVEPRRVGSSRA----LVPRNAQKFHTEDVLYLESPDFEQDMRSGVLT 291
 QY 311 AGRACSSSSALGCCELCCGGRGHRTRTWRVFCNOTEWCIVSNSRNTHTRIHEC 369
 Db 292 RGRICKTSKTAIDGCCLCGCGFHTAQVELAERCSCFKWCVKQFCORLVHLTC 350
 DR EMBL:AY009496; ARB3658 1; -->
 DR EMBL:AF316943; ARB51699 1; -->
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 DR PRINTS:PRO134; WNPOTEN.
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 FT SIGNAL 1
 FT CHAIN 23 351
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 OY 14 TLLALAAKPLAANSRGWGINVASSNLITLSKQIVLVEPSQLRSKRFLR 73
 Db 9 SRLRYFAVESSAARN----WLYLAKLSSVSISETICE---KLKGIIQVQMK 58
 QY 74 QPGILHSVSGLOSSAREKFGNFRNRCNTAPFPHSKINNGREFAFIATSA 133
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 Db 179 ASSRALMHNNEAGKALTHMRVECKHGVSGSTEWTKPAPFRRQGHAIKEF 238
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 Db 239 DATEVEPRRVGSSRA----LVPRNAQKFHTEDVLYLESPDFEQDMRSGVLT 291
 QY 311 AGRACSSSSALGCCELCCGGRGHRTRTWRVFCNOTEWCIVSNSRNTHTRIHEC 369
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 OY 14 TLLALAAKPLAANSRGWGINVASSNLITLSKQIVLVEPSQLRSKRFLR 73
 Db 9 SRLRYFAVESSAARN----WLYLAKLSSVSISETICE---KLKGIIQVQMK 58
 QY 74 QPGILHSVSGLOSSAREKFGNFRNRCNTAPFPHSKINNGREFAFIATSA 133
 Db 119 GVAFAVTRACSSSELEKGCRTVQGVSQGCSJSUNIAYVAWSQEDVRSKG 178
 QY 193 -DLRFELNHNNNEAGRITVSEMPQCCHNSGSTVTCRMLPFLRAWDYLDRP 250
 Db 179 ASSRALMHNNEAGKALTHMRVECKHGVSGSTEWTKPAPFRRQGHAIKEF 238
 QY 251 DRSKFLYGRGSGRASHAELRLPEDAHFPHSPHDLYFEESPNTGYSRGTATI 310
 Db 239 DATEVEPRRVGSSRA----LVPRNAQKFHTEDVLYLESPDFEQDMRSGVLT 291
 QY 311 AGRACSSSSALGCCELCCGGRGHRTRTWRVFCNOTEWCIVSNSRNTHTRIHEC 369
 Db 292 RGRICKTSKTAIDGCCLCGCGFHTAQVELAERCSCFKWCVKQFCORLVHLTC 350
 DR EMBL:AY009496; ARB3658 1; -->
 DR EMBL:AF316943; ARB51699 1; -->
 DR EMBL:AL031281; CAB5201 1; -->
 DR EMBL:AF335591; ARK25765 1; -->
 DR EMBL:AK03657; ARS5042 1; -->
 DR GenBank:HGNC:12283; WNT4
 DR InterPro:IPR000970; Wnt_gtfactor.
 DR PTam:PF00110; wnt_1.
 DR PRINTS:PRO134; WNPOTEN.
 DR SMART:SM00097; WNT1 1.
 DR Developmental protein; Glycoprotein; Signal.
 FT SIGNAL 1
 FT CHAIN 23 351
 FT CARBOHYD 88 88
 FT CARBOHYD 297 297 N-LINKED (GLCNAC -> -) (POTENTIAL).
 SF SEQUENCE 351 AA; 35049 MW: 7675C739E9B9D9 CRC64:
 Query Match 41.1%; Score 836; DB 1; Length 351;
 Best Local Similarity 44.6%; Pred. No. 1 1e-65; DB 1; Length 351;
 Matches 160; Conservative 55; Mismatches 124; Idents 20; Gaps 1;
 OY 14 TLLALAAKPLAANSRGWGINVASSNLITLSKQIVLVEPSQLRSKRFLR 73
 Db 9 SRLRYFAVESSAARN----WLYLAKLSSVSISETICE---KLKGIIQVQMK 58
 QY 74 QPGILHSVSGLOSSAREKFGNFRNRCNTAPFPHSKINNGREFAFIATSA 133
 Db 119 GVAFAVTRACSSSELEKGCRTVQGVSQGCSJSUNIAYVAWSQEDVRSKG 178
 QY 193 -DLRFELNHNNNEAGRITVSEMPQCCHNSGSTVTCRMLPFLRAWDYLDRP 250
 Db 179 ASSRALMHNNEAGKALTHMRVECKHGVSGSTEWTKPAPFRRQGHAIKEF 238
 QY 251 DRSKFLYGRGSGRASHAELRLPEDAHFPHSPHDLYFEESPNTGYSRGTATI 310
 Db 239 DATEVEPRRVGSSRA----LVPRNAQKFHTEDVLYLESPDFEQDMRSGVLT 291
 QY 311 AGRACSSSSALGCCELCCGGRGHRTRTWRVFCNOTEWCIVSNSRNTHTRIHEC 369
 Db 292 RGRICKTSKTAIDGCCLCGCGFHTAQVELAERCSCFKWCVKQFCORLVHLTC 350
 DR EMBL:AY009496; ARB3658 1; -->
 DR EMBL:AF316943; ARB51699 1; -->
 DR EMBL:AL031281; CAB5201 1; -->
 DR EMBL:AF335591; ARK25765 1; -->
 DR EMBL:AK03657; ARS5042 1; -->
 DR GenBank:HGNC:12283; WNT4
 DR InterPro:IPR000970; Wnt_gtfactor.
 DR PTam:PF00110; wnt_1.
 DR PRINTS:PRO134; WNPOTEN.
 DR SMART:SM00097; WNT1 1.
 DR Developmental protein; Glycoprotein; Signal.
 FT SIGNAL 1
 FT CHAIN 23 351
 FT CARBOHYD 88 88
 FT CARBOHYD 297 297 N-LINKED (GLCNAC -> -) (POTENTIAL).
 SF SEQUENCE 351 AA; 35049 MW: 7675C739E9B9D9 CRC64:
 Query Match 41.1%; Score 836; DB 1; Length 351;
 Best Local Similarity 44.6%; Pred. No. 1 1e-65; DB 1; Length 351;
 Matches 160; Conservative 55; Mismatches 124; Idents 20; Gaps 1;
 OY 14 TLLALAAKPLAANSRGWGINVASSNLITLSKQIVLVEPSQLRSKRFLR 73
 Db 9 SRLRYFAVESSAARN----WLYLAKLSSVSISETICE---KLKGIIQVQMK 58
 QY 74 QPGILHSVSGLOSSAREKFGNFRNRCNTAPFPHSKINNGREFAFIATSA 133
 Db 119 GVAFAVTRACSSSELEKGCRTVQGVSQGCSJSUNIAYVAWSQEDVRSKG 178
 QY 193 -DLRFELNHNNNEAGRITVSEMPQCCHNSGSTVTCRMLPFLRAWDYLDRP 250
 Db 179 ASSRALMHNNEAGKALTHMRVECKHGVSGSTEWTKPAPFRRQGHAIKEF 238
 QY 251 DRSKFLYGRGSGRASHAELRLPEDAHFPHSPHDLYFEESPNTGYSRGTATI 310
 Db 239 DATEVEPRRVGSSRA----LVPRNAQKFHTEDVLYLESPDFEQDMRSGVLT 291
 QY 311 AGRACSSSSALGCCELCCGGRGHRTRTWRVFCNOTEWCIVSNSRNTHTRIHEC 369
 Db 292 RGRICKTSKTAIDGCCLCGCGFHTAQVELAERCSCFKWCVKQFCORLVHLTC 350
 DR EMBL:AY009496; ARB3658 1; -->
 DR EMBL:AF316943; ARB51699 1; -->
 DR EMBL:AL031281; CAB5201 1; -->
 DR EMBL:AF335591; ARK25765 1; -->
 DR EMBL:AK03657; ARS5042 1; -->
 DR GenBank:HGNC:12283; WNT4
 DR InterPro:IPR000970; Wnt_gtfactor.
 DR PTam:PF00110; wnt_1.
 DR PRINTS:PRO134; WNPOTEN.
 DR SMART:SM00097; WNT1 1.
 DR Developmental protein; Glycoprotein; Signal.
 FT SIGNAL 1
 FT CHAIN 23 351
 FT CARBOHYD 88 88
 FT CARBOHYD 297 297 N-LINKED (GLCNAC -> -) (POTENTIAL).
 SF SEQUENCE 351 AA; 35049 MW: 7675C739E9B9D9 CRC64:
 Query Match 41.1%; Score 836; DB 1; Length 351;
 Best Local Similarity 44.6%; Pred. No. 1 1e-65; DB 1; Length 351;
 Matches 160; Conservative 55; Mismatches 124; Idents 20; Gaps 1;
 OY 14 TLLALAAKPLAANSRGWGINVASSNLITLSKQIVLVEPSQLRSKRFLR 73
 Db 9 SRLRYFAVESSAARN----WLYLAKLSSVSISETICE---KLKGIIQVQMK 58
 QY 74 QPGILHSVSGLOSSAREKFGN

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Search completed: April 22, 2003, 16:39:47
Job time : 26 secs

GenCore version 5.1.4-P5.4578
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OM protein - protein search, using sw model

Run on: April 22, 2003, 16:36:48 : Search time 87 seconds
(without alignments)
876,292 Million cell updates/sec

Title: US-09-674-292-1
Perfect score: 2035
Sequence: 1 MGILWALLPGWVSATILLALA.....WCYHRVSCRNCHTRVHLHECL 370

Scoring table: BL20SM62
Gapop 10.0 , Gapext. 0.5

Searched: 671580 seqs, 20604715 residues

Total number of bits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%, Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_21;*

- 1: SP_acachea;*
- 2: SP_bacteria;*
- 3: SP_fungi;*
- 4: SP_human;*
- 5: SP_invertebrate;*
- 6: SP_mammal;*
- 7: SP_micr;*
- 8: SP_ornamele;*
- 9: SP_phage;*
- 10: SP_plant;*
- 11: SP_protein;*
- 12: SP_virus;*
- 13: SP_vertebrate;*
- 14: SP_unclassified;*
- 15: SP_virus;*
- 16: SP_bacteriap;*
- 17: SP_archeap;*

Pred No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

*** SUMMARIES**

ALIGMENTS

Result No.	Score	Query	Match Length	DB ID	Description
1	159.8	78.5	370	13 P79752	P79752 fugu rubripinnis
2	123.5	59.1	262	13 Q9PTT9	Q9PTT9 oryzae latifolia
3	115.1	56.5	394	5 OGKR6	OGKR6 griffithsia bimaculata
4	1127.5	55.4	374	5 Q8T96	Q8T96 cyprienius
5	1054.5	52.3	377	5 Q61699	Q61699 branchiostoma
6	878.5	43.1	505	OGWRF7	OGWRF7 muscidium coeruleum
7	866.5	42.6	303	5 Q9TX64	Q9TX64 tribolium castaneum
8	834	41.0	353	5 Q9T26	Q9T26 branchiostoma
9	818	40.2	375	13 Q9PHR1	Q9PHR1 gallus gallus
10	800.5	39.3	395	5 Q8WS75	Q8WS75 branchiostoma
11	785	38.6	360	11 Q9CWX3	Q9CWX3 mus musculus
12	783	38.5	358	13 Q9IAU3	Q9IAU3 brachydanio
13	779	38.3	350	13 Q8UR97	Q8UR97 fugu rubripinnis
14	774.5	38.0	13 Q9BSN7	Q9BSN7 gallus gallus	
15	768.5	37.7	380	11 Q8VQV6	Q8VQV6 mus musculus
15	767	37.7	250	5 Q27671	Q27671 junonia coenia

Query Match 78.5%; Score 159.8; Lk 370; Search 370;
Best Local Similarity 78.5%; Freql. No. 671580;
Matches 282; Conservative 41; Mismatches 42; Deletions 2; Gaps 2;
QY ALI-GWVSATILLALA.....WCYHRVSCRNCHTRVHLHECL 370;
SEQUENCE 370 AA: 41953 MW: DECC1B685CEEE2 C9-C4;

Db	352	RTEMTERKCHCQFHGCCYVTCQECQRKHQHTC	344	QY	121	CRETAFFATTSAGVTHSVARST-SEGSETECTYERRPGP;P- WHYGSUNILFG	177
RESULT	11			QY	105	SKESEPVWAISSAGVWFAITRACQSQELKSCDJKKGSAKISK;P- WHYGSUNILFG	164
ID	Q9C2W3	PRELIMINARY;	PRT;	QY	178	RIFGEEFVSGE-KGULRILMHNHEAGITIVSEMPOEICH-MJSNTVCPHIL	236
AC	Q9C2W3;			QY	179	IKFATAFVIAKEURKGDKARMLNHNHEAGIKAVERFLQECK-BHWSJSCTTICLAM	224
DT	01-JUN-2001	(TREMBrel. 17, Created)		QY	237	PTLAVIGVLRDFGASRMLYGRGSNRASHAEILRFEGAKG-SEPMVWFSF	296
DT	01-JUN-2001	(TREMBrel. 17, Last sequence update)		QY	225	AUFKTDGLWRYKNGIAUWMQDSTG-----FIVANKRKFPTKNLWYFENSP	275
DE	2610510E18Rik	protein (wingless-related MMTV integration site 2).		QY	297	NFCYSGRLGTTAGACGSSSIALGCGCCRGHETRQVTE-CMTHCHVS	356
GN	Mus musculus (Mouse)			QY	276	DYCIRUREAGSLGTAGRCVNLTSRGMSCEVMCCGRGYUTSHWTRM-KCCKPHWCAV	335
OC	bakayota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			QY	357	CRNCIHLHEC 369	
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			QY	336	CQCLEALWHTC 345	
RN	[1]			QY	121	i	
RP	SEQUENCE FROM N.A.			QY	105	i	
RC	STRAIN=C7BL6j; TISSUE=EMBRYO;			QY	178	i	
RX	MEDLINE=21088660; PubMed=11217851;			QY	179	i	
RA	Kawai J., Shitagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,			QY	237	i	
RA	Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,			QY	225	i	
RA	Aizawa K., Iizawa M., Nishi K., Kiyosawa H., Kondo S., Yamamoto T.,			QY	297	i	
RA	Kadota K., Matsuda H.A., Ashburner M., Baralow S., Casavant T.,			QY	276	i	
RA	Fleischmann K., Gadsden T., Gissi C., King B., Kocikwa H.,			QY	357	i	
RA	Koehl P., Lewis S., Matsumoto Y., Nikaido I., Resole G., Quackenbush J.,			QY	336	i	
RA	Schriml L.M., Staabli F., Suzuki R., Tonira M., Wagner T., Wastie M.,			QY	121	i	
RA	Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,			QY	105	i	
RA	Blake J., Bottelli D., Bojunga N., Carrascal J., de Bonaldo M.F.,			QY	178	i	
RA	Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,			QY	179	i	
RA	Gustincich S., Hill D., Hofmann M., Huone D.A., Kamoya M., Lee N.H.,			QY	237	i	
RA	Lyons P., Marchionni L., Mashina J., Mazzarelli J., Monbarros P.,			QY	225	i	
RA	Nardone P., Ring B., Ringwald M., Rodriguez J., Sakamoo N.,			QY	297	i	
RA	Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,			QY	276	i	
RA	Suzuki H., Toyooka K., Wang K.H., Weitz S., Wittraker C., Wu Ming L.,			QY	357	i	
RA	Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsuki S.,			QY	336	i	
RA	Hayashizaki Y.,			QY	121	i	
RT	Functional annotation of a full-length mouse cDNA collection";			QY	105	i	
RL	Nature 409;885-890(2001).			QY	178	i	
RN	[2]			QY	179	i	
RP	SEQUENCE FROM N.A.			QY	237	i	
RC	TISSUE=LIVER;			QY	225	i	
RA	Straussberg R.;			QY	297	i	
RL	Submitted (PRB=2002) to the EMBL/GenBank/DBJ databases.			QY	276	i	
CC	-- FUNCTION: PROBABLE DEVELOPMENTAL PROTEIN (BY SIMILARITY).			QY	357	i	
CC	-- SUBCELLULAR LOCATION: POSSIBLY SECRETED AND ASSOCIATES WITH THE EXTRACELLULAR MATRIX (BY SIMILARITY).			QY	336	i	
CC	-- SIMILARITY: BELONGS TO THE WNT FAMILY.			QY	121	i	
EMBL	AK012953; BAB8025.1; --;			QY	105	i	
EMBL	BC026373; AAH6373.1; --;			QY	178	i	
MOD	MGII-1919405; 2610510E18Rik			QY	179	i	
DR	InterPro:IPR000970; Wnt1_glythiactor.			QY	237	i	
DR	PRINTS: PRO134; WNPFPTEIN.			QY	225	i	
DR	SMART: SM0097; WNT1.			QY	297	i	
DR	PROSITE: PS00246; WNT1; I-			QY	276	i	
KW	developmental protein; glycoprotein.			QY	357	i	
SEQUENCE	360 AA; 40482 MW; 5E376445381; SEAD CRG64;			QY	336	i	
SO	SEQUENCE	358 AA; 39209 MW; 78A6B4B00844C44		QY	121	i	
Query Match	38 68%; Score 785; DB 11; Length 360;			QY	105	i	
Best Local Similarity	39 59%; Pred. No. 2; se=67;			QY	178	i	
Matches	149; Conservative 65; Mismatches 123; Indels 36; Gaps 7;			QY	179	i	
Matrices	158; Conservative 49; Mismatches 129; Insert 25; Gaps 7;			QY	237	i	
QY	2 GLWALLPGWVATLALAAALPAALANSSGRGMJVNVVASSNLTUDSKLSLQVLEPL 61			QY	15	i	
QY	1 GIWILWPL-----LLTM-----LTPESSWVMEATGSSRWCMD-----NV 44			QY	14	i	
QY	62 OLISRKKRTRONGGIGHSVSGGLOSARVECKQFRNRKRNCPATAPGRH-LFGKIVNG 120			QY	132	i	
Db	45 PGLVSRQROLGHRHPDVWRAIGVWAEWTECQHQFRHRANCNTLDKDHISLGVLRS 104			QY	122	i	
Db	192 RDL--FELMINHNNHEAGRTT-SEMRGECKWSMSCTVTCM-IZLAVGVRL 248			QY	192	i	

Db	182 KGMSSGRPLMNHNNEAGRKAHLHNNOVECKCHGVSSCSELRTCKWMPFERRVGAVLKE 241	Db	228 TGDHFKKRYNGAVVNVNGYGTFT-----AHARKEGKSRVLEDPDY 275
QY	249 RFDGASRVLGNRGNRASRAELRLRPEPEPAHPPPSFHDLYFFKSPNFCYSGRUGTA 308	QY	294 CTYSQRGLTAGFRAGNCNSSPALGSELLCGCHRHTKATTCNTIFHMCVSCR 358
Db	242 HFDGATEPKTRFVGETA-----LIPROPVWPEAFRLVYLSPERFLDFNIP 294	Db	276 CYRQDOSLSLIGJGMCNRISPTGIDCWMGCGYDTSRNPNTKZERFHCAVLR 335
QY	309 GTACRACNSSS-ALEGCLLGGRSHTRTUFPTERONGFHWCHNSRCNTHIVLH 367	QY	359 NCTHTRVABEC 369
Db	295 GIARRCNCTSPLADGEELLOGPESRAEVAWVORSCSWSQSVQCKNVLH 354	Db	336 DCHQ2WVWHTC 346
QY	368 EC 369		
Db	355 TC 356;		
	RESULT 13		
	Q8W39 PRELIMINARY; PRT: 350 AA.		
	Q8UW9 PRELIMINARY; PRT: 350 AA.		
AC	08UW9; DT 01-MAR-2002 (TREMBL: 20; Created)		
DT	01-MAR-2002 (TREMBL: 20; Last sequence update)		
DT	01-JUN-2002 (TREMBL: 21; Last annotation update)		
DE	WNT2 protein.		
GN	WNT2.		
DS	Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostei;		
OC	Actinopterygii; Neopteri; Teleostei; Neoteleostei;		
OC	Acanthopterygii; Telecomorphia; Tetraodontiformes;		
OC	Tetraodontidae; Takifugu.		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Ayelle K., Beckstrom-Sternberg S.M., Benjamin B., Blakesley R.W., Bouffard G.G., Green K., Brinkley C., Brooks S., Dietrich N.L., Granite S., Guan X., Gupta J., Ho S.-L., Itoh J.R., Karlin S., Lee-Lin S.-Q., Legapri R., Lim M., Nadiro G.L., Maturo V.B., Masiello C., Mastrian S.D., McCloskey J.C., McDowell J., Pearson R., Prasad A., Shevchenko Y., Snyder B., Stantripop S., Thomas J.W., Thomas P.J., Touhami J.W., Turgeon C., Vogt J.L., Walker M.A., Wetherby K.D., Zhang L.-H., Green E.D.		
RT	"NISC Comparative Sequencing Initiative."		
RL	Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.		
DR	EMBL: AC09127; RAL4358_1; RAL4358_2; RAL4358_3; RAL4358_4; RAL4358_5; RAL4358_6; RAL4358_7; RAL4358_8; RAL4358_9; RAL4358_10; RAL4358_11; RAL4358_12; RAL4358_13; RAL4358_14; RAL4358_15; RAL4358_16; RAL4358_17; RAL4358_18; RAL4358_19; RAL4358_20; RAL4358_21; RAL4358_22; RAL4358_23; RAL4358_24; RAL4358_25; RAL4358_26; RAL4358_27; RAL4358_28; RAL4358_29; RAL4358_30; RAL4358_31; RAL4358_32; RAL4358_33; RAL4358_34; RAL4358_35; RAL4358_36; RAL4358_37; RAL4358_38; RAL4358_39; RAL4358_40; RAL4358_41; RAL4358_42; RAL4358_43; RAL4358_44; RAL4358_45; RAL4358_46; RAL4358_47; RAL4358_48; RAL4358_49; RAL4358_50; RAL4358_51; RAL4358_52; RAL4358_53; RAL4358_54; RAL4358_55; RAL4358_56; RAL4358_57; RAL4358_58; RAL4358_59; RAL4358_60; RAL4358_61; RAL4358_62; RAL4358_63; RAL4358_64; RAL4358_65; RAL4358_66; RAL4358_67; RAL4358_68; RAL4358_69; RAL4358_70; RAL4358_71; RAL4358_72; RAL4358_73; RAL4358_74; RAL4358_75; RAL4358_76; RAL4358_77; RAL4358_78; RAL4358_79; RAL4358_80; RAL4358_81; RAL4358_82; RAL4358_83; 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